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STIC Database Tracking Number: 218750

TO: Patricia Duffy
Location: REM-3B05&3C18
Art Unit: 1645
Thursday, March 29, 2007
Case Serial Number: 10/063549

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

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218750

STIC-Biotech/ChemLib

From: Duffy, Patricia
Sent: Tuesday, March 20, 2007 12:03 PM
To: STIC-Biotech/ChemLib
Subject: spdi search

Dear Stic,

03-1047

IN re:10/063,549
Please search SEQ ID NO:46.
SPDI search.

135 AA

CRFE

Patricia A. Duffy, Ph.D.
Primary Patent Examiner
571-272-0855,
Remsen 3B05,
Mailbox: 3C18

72448

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OM protein - protein search, using sw model

Run on:     March 29, 2007, 02:21:58 ; Search time 82 Seconds
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Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2097797 seqs, 46214858 residues

Total number of hits satisfying chosen parameters:    2097797

Minimum DB seq length: 0
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Post-processing: Minimum Match Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
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              GenCore version 6.2
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Total number of hits satisfying chosen parameters:       938351

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.
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SUMMARIES

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29	312.5	17.6	329	6	US-10-669-920-751	Sequence 751, App
30	264	14.9	269	6	US-10-669-920-753	Sequence 753, App
31	262	14.8	314	6	US-10-405-027-4324	Sequence 4324, Ap
32	260	14.7	315	6	US-10-669-920-755	Sequence 755, App
33	238.5	13.5	423	6	US-10-533-520-3182	Sequence 3182, Ap
34	226.5	12.8	329	6	US-10-669-920-748	Sequence 748, App
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37	182.5	10.3	335	6	US-10-533-520-6249	Sequence 6249, Ap
38	182.5	10.3	335	7	US-11-537-686-3	Sequence 3, Appli
39	182.5	10.3	335	7	US-11-066-316A-947	Sequence 947, App
40	170	9.6	365	6	US-10-533-519-2361	Sequence 2361, App
41	170	9.6	365	7	US-11-371-354-68099	Sequence 68099, A
42	168	9.5	293	6	US-10-405-027-3601	Sequence 3601, Ap
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44	150.5	8.5	285	6	US-10-405-027-3148	Sequence 3148, Ap
45	150.5	8.5	285	6	US-10-405-027-3179	Sequence 3179, Ap
46	150.5	8.5	285	6	US-10-405-027-4447	Sequence 4447, Ap
47	150.5	8.5	285	6	US-10-405-027-4448	Sequence 4448, Ap
48	150.5	8.5	285	6	US-10-796-280-1289	Sequence 1289, Ap
49	150.5	8.5	285	6	US-11-363-149-82	Sequence 82, Appl
50	150.5	8.5	285	6	US-11-363-151-82	Sequence 82, Appl
51	150.5	8.5	285	6	US-11-429-276-444	Sequence 444, App
52	150.5	8.5	285	6	US-11-455-366-12	Sequence 12, Appl
53	150.5	8.5	285	6	US-11-386-937-9	Sequence 9, Appli
54	150.5	8.5	285	6	US-11-429-373-444	Sequence 444, App
55	150.5	8.5	285	6	US-11-386-836-9	Sequence 9, Appli
56	150.5	8.5	285	6	US-11-537-686-2	Sequence 2, Appli
57	145	8.2	211	6	US-10-777-288A-3760	Sequence 3760, Ap
58	142	8.0	367	6	US-10-760-320A-2518	Sequence 2518, Ap
59	141	8.0	149	6	US-10-866-878-571	Sequence 571, App
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153	102.5	5.8	519	7	US-11-154-977-31	Sequence 31, Appl
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595	81	4.6	3493	US-11-063-439-35	7	Sequence 35, Appl
596	81	4.6	3493	US-11-063-439-47	7	Sequence 47, Appl
597	81	4.6	3493	US-11-064-247-6	7	Sequence 6, Appli
598	81	4.6	3493	US-11-064-247-12	7	Sequence 12, Appl
599	81	4.6	3493	US-11-064-247-35	7	Sequence 35, Appl
600	81	4.6	3493	US-11-064-247-47	7	Sequence 47, Appl
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602	81	4.6	3494	US-11-063-439-104	7	Sequence 104, App
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611	80.5	4.5	205	US-10-405-027-3621	6	Sequence 3621, Ap
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625	80.5	4.5	346	US-11-500-508-438	7	Sequence 438, App
626	80.5	4.5	346	US-11-500-508-439	7	Sequence 439, App
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635	80.5	4.5	411	US-11-241-607-3638	7	Sequence 3638, Ap
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637	80.5	4.5	617	US-11-317-786B-32	7	Sequence 32, Appl
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640	80.5	4.5	721	US-10-530-643-233	6	Sequence 233, App
641	80.5	4.5	721	US-10-530-643-235	6	Sequence 235, App
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656	80	4.5	528	US-11-459-845-20	7	Sequence 20, Appl
657	80	4.5	528	US-11-499-835-71	7	Sequence 71, Appl
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667	80	4.5	3485	US-11-064-247-76	7	Sequence 76, Appl
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670	80	4.5	3502	US-11-063-439-275	7	Sequence 275, App
671	80	4.5	3503	US-11-064-247-275	7	Sequence 275, App
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673	80	4.5	3503	US-11-064-247-23	7	Sequence 23, Appl
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676	79.5	4.5	335	US-11-594-148-36	7	Sequence 36, Appl
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688	79.5	4.5	1465	US-10-219-051B-1832	6	Sequence 1832, Ap
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690	79	4.5	260	US-11-001-793-7407	7	Sequence 7407, Ap
691	79	4.5	278	US-11-486-345-6	7	Sequence 6, Appli
692	79	4.5	305	US-11-486-345-34	7	Sequence 34, Appl
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702	4.5	79	492	7	US-11-493-132-30	Sequence 30, Appl
703	4.5	79	495	7	US-11-493-132-26	Sequence 26, Appl
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842	4.3	77	4834	6	US-10-505-928-827	Sequence 827, App
843	4.3	76.5	364	6	US-10-511-937-2927	Sequence 2927, Ap
844	4.3	76.5	364	7	US-10-325-899-9381	Sequence 9381, App
845	4.3	76.5	426	6	US-10-219-051B-59659	Sequence 59659, A
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849	76.5	4.3	560	6	US-10-953-349-3923	Sequence 3923, Ap
850	76.5	4.3	659	6	US-10-449-902-38329	Sequence 38329
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852	76.5	4.3	830	7	US-11-056-355B-80621	Sequence 80621, A
853	76.5	4.3	876	7	US-11-056-355B-80620	Sequence 80620, A
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855	76.5	4.3	1089	7	US-10-796-307-672	Sequence 672, App
856	76.5	4.3	1089	7	US-11-248-956-22	Sequence 22, Appl
857	76.5	4.3	1089	7	US-11-365-989-130	Sequence 130, App
858	76.5	4.3	1089	7	US-11-401-340-14	Sequence 14, Appl
859	76.5	4.3	1089	6	US-11-129-740-275	Sequence 275, Ap
860	76.5	4.3	1124	6	US-10-529-348-2433	Sequence 2433, Ap
861	76.5	4.3	1124	6	US-10-533-520-1961	Sequence 1961, Ap
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865	76.5	4.3	1251	7	US-11-166-372-2641	Sequence 2641, Ap
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872	76	4.3	357	7	US-11-218-141-2969	Sequence 2969, Ap
873	76	4.3	377	7	US-11-330-403-7428	Sequence 7428, Ap
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893	75.5	4.3	280	7	US-11-229-307-13	Sequence 13, Appl
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955	75	4.2	543	6	US-10-743-643-2283	Sequence 2283, Ap
956	75	4.2	641	6	US-11-039-643-26	Sequence 26, Appl
957	75	4.2	858	7	US-11-389-543-343	Sequence 343, App
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974	75	4.2	3396	6	US-10-700-439-118	Sequence 233, App
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980	75	4.2	3512	7	US-11-064-247-34	Sequence 72, Appl
981	75	4.2	3512	7	US-11-064-247-72	Sequence 99, Appl
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984	75	4.2	3528	7	US-11-063-439-32	Sequence 32, Appl
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988	74.5	4.2	261	7	US-11-386-937-12	Sequence 12, Appl
989	74.5	4.2	261	7	US-11-386-836-12	Sequence 10191, A
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1344	6	629	4.0	71.5	Sequence 76771, A	US-11-056-355B-76771
1345	7	666	4.0	71.5	Sequence 50283, A	US-11-241-607-50283
1346	7	675	4.0	71.5	Sequence 749, App	US-11-366-965-749
1347	6	733	4.0	71.5	Sequence 54676, A	US-11-520-715-54676
1348	7	764	4.0	71.5	Sequence 2050, Ap	US-10-219-051B-2050
1349	6	766	4.0	71.5	Sequence 2054, Ap	US-10-219-051B-2054
1350	6	822	4.0	71.5	Sequence 65, Appl	US-11-191-244-65
1351	6	822	4.0	71.5	Sequence 44105, A	US-10-449-902-44105
1352	7	865	4.0	71.5	Sequence 96337, A	US-11-056-355B-96337
1353	7	921	4.0	71.5	Sequence 47408, A	US-11-241-607-47408
1354	7	944	4.0	71.5	Sequence 54509, A	US-10-449-902-54509
1355	7	944	4.0	71.5	Sequence 157, Appl	US-11-450-517-157
1356	7	945	4.0	71.5	Sequence 96336, A	US-11-056-355B-96336
1357	7	944	4.0	71.5	Sequence 47407, A	US-11-241-607-47407
1358	7	944	4.0	71.5	Sequence 2739, Ap	US-11-293-697-2739
1359	7	945	4.0	71.5		

Right block (lines 1360–1434)

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1360	71.5	4.0	946	US-11-056-355B-96335	Sequence 96335, A
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1362	71.5	4.0	962	US-10-570-909-49	Sequence 49, Appl
1363	71.5	4.0	1114	US-10-527-101-24	Sequence 24, Appl
1364	71.5	4.0	1114	US-10-529-348-1536	Sequence 1536, Ap
1367	71.5	4.0	1115	US-10-529-348-1650	Sequence 1650, Ap
1368	71.5	4.0	1165	US-11-066-316A-1088	Sequence 1088, Ap
1369	71.5	4.0	1405	US-10-603-113-18103	Sequence 18103, A
1370	71.5	4.0	2468	US-10-219-051B-8648	Sequence 8648, Ap
1371	71.5	4.0	2468	US-10-219-051B-8652	Sequence 8652, Ap
1372	71.5	4.0	2468	US-10-219-051B-8656	Sequence 8656, Ap
1373	71.5	4.0	2468	US-10-219-051B-8660	Sequence 8660, Ap
1374	71.5	4.0	2527	US-10-529-348-1654	Sequence 1654, Ap
1375	71.5	4.0		US-10-529-348-955	Sequence 955, App
1376	71	4.0	165	US-10-703-032-134881	Sequence 134881,
1377	71	4.0	200	US-11-486-448-109007	Sequence 109007,
1378	71	4.0	233	US-11-366-942-244	Sequence 244, App
1379	71	4.0	283	US-10-449-902-50910	Sequence 50910, A
1380	71	4.0	283	US-11-293-697-4639	Sequence 4639, Ap
1381	71	4.0	296	US-11-332-037-267	Sequence 267, App
1382	71	4.0	296	US-11-332-037-280	Sequence 280, App
1383	71	4.0	344	US-10-743-643-193	Sequence 193, App
1384	71	4.0	345	US-11-090-997-188	Sequence 188, App
1385	71	4.0	365	US-11-129-740-102	Sequence 102, App
1386	71	4.0	382	US-11-520-715-51918	Sequence 51918, A
1387	71	4.0	387	US-11-293-697-3214	Sequence 3214, Ap
1388	71	4.0	422	US-11-520-715-64538	Sequence 64538, A
1389	71	4.0	425	US-10-760-320A-3449	Sequence 3449, Ap
1390	71	4.0	436	US-10-449-902-49218	Sequence 49218, A
1391	71	4.0	436	US-11-129-740-101	Sequence 101, App
1392	71	4.0	455	US-10-953-349-8354	Sequence 8354, Ap
1393	71	4.0	455	US-11-056-355B-25941	Sequence 25941, A
1394	71	4.0	455	US-11-056-355B-102693	Sequence 102693,
1395	71	4.0	455	US-11-056-355B-113932	Sequence 113932,
1396	71	4.0	462	US-11-241-607-3285	Sequence 3285, Ap
1397	71	4.0	462	US-10-953-349-8353	Sequence 8353, Ap
1398	71	4.0	462	US-11-056-355B-25940	Sequence 25940, A
1399	71	4.0	462	US-11-056-355B-102692	Sequence 102692,
1400	71	4.0	464	US-11-056-355B-113931	Sequence 113931,
1401	71	4.0	464	US-11-241-607-3284	Sequence 3284, Ap
1402	71	4.0	479	US-11-241-607-3806	Sequence 3806, Ap
1403	71	4.0	482	US-11-371-354-12564	Sequence 12564, A
1404	71	4.0	482	US-11-371-354-57789	Sequence 57789, A
1405	71	4.0	487	US-11-371-354-76501	Sequence 76501, A
1406	71	4.0	487	US-11-129-740-110	Sequence 110, App
1407	71	4.0	487	US-11-056-355B-102691	Sequence 102691,
1408	71	4.0	492	US-11-056-355B-113930	Sequence 113930,
1409	71	4.0	492	US-11-241-607-3805	Sequence 3805, Ap
1410	71	4.0	492	US-10-953-349-8352	Sequence 8352, Ap
1411	71	4.0	492	US-11-056-355B-25939	Sequence 25939, A
1412	71	4.0	523	US-11-241-607-53749	Sequence 53749, A
1413	71	4.0	524	US-11-129-740-100	Sequence 100, App
1414	71	4.0	524	US-11-233-089-44	Sequence 44, Appl
1415	71	4.0	541	US-10-603-113-14463	Sequence 14463, A
1416	71	4.0	551	US-11-499-835-63	Sequence 63, Appl
1417	71	4.0	621	US-11-375-523-12	Sequence 12, Appl
1418	71	4.0	649	US-11-226-554-90	Sequence 90, Appl
1419	71	4.0	661	US-11-248-718-90	Sequence 90, Appl
1420	71	4.0	671	US-11-538-552-90	Sequence 90, Appl
1421	71	4.0	671	US-11-499-835-61	Sequence 61, Appl
1422	71	4.0	671	US-11-241-607-47257	Sequence 47257, A
1423	71	4.0	673	US-10-508-580-9	Sequence 9, Appli
1432	71	4.0	687	US-10-548-569-2	Sequence 2, Appli
1433	71	4.0	687	US-11-300-928-47	Sequence 47, Appl
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1435	71	4.0	687	7	US-11-375-523-6	Sequence 6, Appli
1436	71	4.0	690	6	US-10-471-571A-1978	Sequence 1978, Ap
1437	71	4.0	691	7	US-11-241-607-47256	Sequence 47256, A
1438	71	4.0	708	6	US-10-526-324-54	Sequence 54, Appl
1439	71	4.0	758	6	US-11-401-340-50	Sequence 50, Appl
1440	71	4.0	779	6	US-10-953-349-40228	Sequence 40228, A
1441	71	4.0	780	7	US-11-375-523-14	Sequence 14, Appl
1442	71	4.0	784	6	US-10-953-349-40227	Sequence 40227, A
1443	71	4.0	821	6	US-10-219-051B-2973	Sequence 2973, Ap
1444	71	4.0	821	6	US-10-219-051B-10879	Sequence 10879, A
1445	71	4.0	821	7	US-11-248-956-8	Sequence 8, Appli
1446	71	4.0	821	7	US-11-401-340-23	Sequence 23, Appl
1447	71	4.0	821	7	US-11-129-740-269	Sequence 269, App
1448	71	4.0	831	7	US-10-953-349-40226	Sequence 40226, A
1449	71	4.0	897	6	US-10-990-328-13681	Sequence 13681, A
1450	71	4.0	911	6	US-10-219-051B-8514	Sequence 8514, Ap
1451	71	4.0	911	7	US-11-226-554-89	Sequence 89, Appl
1452	71	4.0	911	7	US-11-248-718-89	Sequence 89, Appl
1453	71	4.0	911	7	US-11-036-255A-8	Sequence 8, Appli
1454	71	4.0	911	7	US-11-371-354-55327	Sequence 55327, A
1455	71	4.0	911	7	US-11-538-552-89	Sequence 89, Appl
1456	71	4.0	916	6	US-10-990-328-13682	Sequence 13682, A
1457	71	4.0	930	7	US-11-396-565-10	Sequence 10, Appl
1458	71	4.0	930	7	US-11-207-802-5314	Sequence 5314, Ap
1459	71	4.0	930	7	US-11-208-208-5314	Sequence 5314, Ap
1460	71	4.0	940	7	US-11-362-260A-411	Sequence 411, App
1461	71	4.0	940	7	US-11-362-260A-421	Sequence 421, App
1462	71	4.0	940	7	US-11-362-260A-425	Sequence 425, App
1463	71	4.0	940	7	US-11-050-875-1148	Sequence 1148, Ap
1464	71	4.0	1018	7	US-11-339-733-42	Sequence 42, Appl
1465	71	4.0	1259	7	US-11-223-945-40	Sequence 40, Appl
1466	71	4.0	1297	6	US-10-533-519-1743	Sequence 1743, Ap
1467	71	4.0	1338	6	US-10-505-928-634	Sequence 634, App
1468	71	4.0	1338	6	US-10-505-928-857	Sequence 857, App
1469	71	4.0	1338	7	US-11-248-956-11	Sequence 11, Appl
1470	71	4.0	1338	7	US-11-365-989-142	Sequence 142, App
1471	71	4.0	1338	7	US-11-401-340-1	Sequence 1, Appli
1472	71	4.0	1338	7	US-11-129-740-282	Sequence 282, App
1473	71	4.0	1338	7	US-11-389-543-185	Sequence 185, App
1474	71	4.0	1338	7	US-11-507-298-4	Sequence 4, Appli
1475	71	4.0	1356	7	US-11-129-740-313	Sequence 313, App
1476	71	4.0	3524	7	US-11-063-439-61	Sequence 61, Appl
1477	71	4.0	3524	7	US-11-064-247-61	Sequence 61, Appl
1478	71	4.0	3528	7	US-11-063-439-38	Sequence 38, Appl
1479	71	4.0	3528	7	US-11-064-247-38	Sequence 38, Appl
1480	71	4.0	3529	7	US-11-063-439-16	Sequence 16, Appl
1481	71	4.0	3529	7	US-11-064-247-16	Sequence 16, Appl
1482	71	4.0	4391	7	US-11-183-325-56	Sequence 56, Appl
1483	71	4.0	4391	7	US-11-592-451-70	Sequence 70, Appl
1484	70.5	4.0	138	6	US-10-703-032-171438	Sequence 171438,
1485	70.5	4.0	162	6	US-10-669-920-406	Sequence 406, App
1486	70.5	4.0	183	6	US-10-664-025-3942	Sequence 3942, Ap
1487	70.5	4.0	235	6	US-10-405-027-4246	Sequence 4246, Ap
1488	70.5	4.0	235	6	US-10-405-027-5638	Sequence 5638, Ap
1489	70.5	4.0	237	6	US-10-569-351-11	Sequence 11, Appl
1490	70.5	4.0	273	6	US-10-574-398-227	Sequence 227, App
1491	70.5	4.0	277	6	US-10-703-032-138149	Sequence 138149,
1492	70.5	4.0	284	7	US-11-371-354-57199	Sequence 57199, A
1493	70.5	4.0	284	7	US-11-241-607-23933	Sequence 23933, A
1494	70.5	4.0	284	7	US-11-241-607-26247	Sequence 26247, A
1495	70.5	4.0	286	6	US-10-219-051B-14311	Sequence 14311, A
1496	70.5	4.0	290	6	US-10-526-324-670	Sequence 670, App
1497	70.5	4.0	298	6	US-11-486-448-60137	Sequence 60137, A
1498	70.5	4.0	318	6	US-10-805-394-5955	Sequence 5955, Ap
1499	70.5	4.0	319	7	US-11-520-715-61202	Sequence 61202, A
1500	70.5	4.0	327	7	US-11-401-340-6	Sequence 6, Appli

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No.	%id	score	length	accession	n	description
103	86	4.9	212	C33258	2	pregnancy-specific
104	86	4.9	354	VGBE67	1	glycoprotein D pre
105	86	4.9	428	I57486	2	pregnancy-specific
106	86	4.9	885	B86257	2	NBS/LRR disease re
107	86	4.9	1327	T09402	2	immunoglobulin-lik
108	85.5	4.8	324	G43354	2	pregnancy-specific
109	85.5	4.8	326	F43354	2	pregnancy-specific
110	85.5	4.8	333	A43354	2	pregnancy-specific
111	85.5	4.8	335	H43354	2	pregnancy-specific
112	85.5	4.8	941	TVMVMD	1	protein-tyrosine k
113	85.5	4.8	2588	T14342	2	NSD1 protein - mou
114	85	4.8	428	JS0032	2	pregnancy-specific
115	85	4.8	731	T16524	2	hypothetical prote
116	85	4.8	757	S48841	1	secretory componen
117	84.5	4.8	656	A96724	2	hypothetical prote
118	84	4.7	275	JC7604	2	CD86 spliced varia
119	84	4.7	851	D90216	2	hypothetical prote
120	84	4.7	1379	S01254	2	hepatocyte growth
121	84	4.7	1499	I50212	1	protein-tyrosine-p
122	84	4.7	3034	T14119	2	seven-pass transme
123	83.5	4.7	315	H71009	2	probable prolifera
124	83.5	4.7	392	T33444	2	hypothetical prote
125	83.5	4.7	656	B49423	2	semaphorin I - fru
126	83.5	4.7	775	T21436	2	hypothetical prote
127	83.5	4.7	1501	I58146	2	protein-tyrosine-p
128	83.5	4.7	1863	S46217	2	protein-tyrosine-p
129	83	4.7	335	A33514	2	pregnancy-specific
130	83	4.7	757	I45956	2	polymeric immunogl
131	83	4.7	873	A49729	1	VLDL receptor prec
132	83	4.7	925	T37475	2	lipoprotein recept
133	83	4.7	1106	T29496	2	hypothetical prote
134	83	4.7	2489	S59782	2	probable membrane
135	82.5	4.7	393	B96780	2	hypothetical prote
136	82.5	4.7	826	B36203	2	iron-responsive el
137	82.5	4.7	1004	A71617	2	SERA antigen/papai
138	82.5	4.7	26926	I38344	1	titin, cardiac mus
139	82	4.6	609	B69666	2	Na+ ABC transporte
140	82	4.6	880	S43009	2	hemagglutinin - ri
141	82	4.6	3562	B53743	2	protein-tyrosine k
142	82	4.6	278	A47171	2	chondroitin sulfat
143	81.5	4.6	352	TDRTOX	1	OX-2 membrane glyc
144	81.5	4.6	355	I77374	2	pregnancy-specific
145	81.5	4.6	378	T06122	2	cysteine proteinas
146	81.5	4.6	497	S00842	2	leukosialin precur
147	81.5	4.6	524	D97264	2	galactose-1-phosph
148	81.5	4.6	708	S44982	2	flagellin - Shigel
149	81.5	4.6	335	T48022	2	hypothetical prote
150	81	4.6	338	B33251	2	nonspecific cross-
151	81	4.6	374	JC4776	2	limbic-system-asso
152	81	4.6	760	S57750	2	naringenin 3-dioxy
153	81	4.5	769	S19374	2	probable membrane
154	81	4.6	829	E97092	2	glycosyltransferas
155	81	4.6	1898	IJHUCP	1	cadherin 3 precurs
156	81	4.6	1941	S46216	2	leukocyte antigen-
157	81	4.5	346	T30554	2	ubiquitin-protein
158	80.5	4.5	376	S46993	2	elk ligand - human
159	80.5	4.5	462	B85435	2	cysteine proteinas
160	80.5	4.5	473	H97292	2	UDP-N-acetylmuramo
161	80.5	4.5	475	AG0612	2	probable transport
162	80.5	4.5	540	I76668	2	pregnancy-specific
163	80.5	4.5	540	B64829	2	membrane protein b
164	80.5	4.5	540	H90751	2	probable transport
165	80.5	4.5	721	F85615	2	probable transport
166	80.5	4.5	823	T09631	2	probable acylamino
167	80.5	4.5	3343	T08092	2	plus fringe glycop
168	80.5	4.5	6642	S44887	2	ZK112.7 protein -
169	80.5	4.5	307	T29757	1	protein UNC-89 - C
170	80	4.5	341	RWMSBC	2	T-cell receptor be
171	80	4.5	343	I61725	2	natural killer ass
172	80	4.5	343	G90680	2	probable periplasm
173	80	4.5	454	C85531	2	periplasmic ferric
174	80	4.5	482	A46532	2	arginine/ornithine
175	80	4.5		JH0110	2	arginine/ornithine

No.	%id	score	length	accession	n	description
176	80	4.5	1040	A49356	2	transient axonal g
177	80	4.5	1170	A40558	2	thrombospondin 1 p
178	79.5	4.5	134	I46627	2	rearranged T-cell
179	79.5	4.5	244	JC8019	1	CD58 protein - pig
180	79.5	4.5	249	A61087	1	myelin P0 glycopro
181	79.5	4.5	273	B28928	2	pregnancy-specific
182	79.5	4.5	275	A28928	2	pregnancy-specific
183	79.5	4.5	282	C28928	2	pregnancy-specific
184	79.5	4.5	289	G90314	2	oxidoreductase lim
185	79.5	4.5	328	JQ1121	2	cysteine proteinas
186	79.5	4.5	400	AI0104	2	probable galactosi
187	79.5	4.5	430	T28143	2	tapasin 1 homolog,
188	79.5	4.5	446	T34782	2	probable signal pe
189	79.5	4.5	490	I41293	2	EcoE type I restri
190	79.5	4.5	769	S16236	2	fibroblast growth
191	79.5	4.5	822	A45081	2	fibroblast growth
192	79.5	4.5	822	A41794	2	keratinocyte growt
193	79.5	4.5	873	I48952	2	VLDL receptor prec
194	79.5	4.5	980	TVCTMD	1	macrophage colony-
195	79.5	4.5	1465	S43529	2	165K protein, skel
196	79.5	4.5	2491	A28372	2	insulin-like growt
197	79	4.5	210	C87256	2	hypothetical prote
198	79	4.5	244	AC1765	2	B. subtilis TagA p
199	79	4.5	438	G64513	2	hypothetical prote
200	79	4.5	479	G84099	2	carboxy-terminal p
201	79	4.5	584	T08678	2	hypothetical prote
202	79	4.5	657	S77543	2	short-chain alcoho
203	79	4.5	903	T20804	2	hypothetical prote
204	79	4.5	1228	G96751	2	hypothetical prote
205	79	4.5	1361	T30884	2	neural specific DN
206	79	4.5	235	S25750	2	Ig lambda chain -
207	78.5	4.4	429	EHRT	1	Ig epsilon chain C
208	78.5	4.4	497	C91225	2	probable oxidoredu
209	78.5	4.4	497	A86072	2	probable oxidoredu
210	78.5	4.4	539	T01513	2	CTP synthase (EC 6
211	78.5	4.4	588	I37202	2	B-CAM protein - hu
212	78.5	4.4	628	I38000	2	Lutheran blood gro
213	78.5	4.4	638	T51383	2	receptor protein k
214	78.5	4.4	831	S39835	2	hypothetical prote
215	78.5	4.4	847	JH0371	2	B-cell adhesion pr
216	78.5	4.4	1036	S22383	2	axonin 1 precursor
217	78.5	4.4	1038	AG2187	2	hypothetical prote
218	78.5	4.4	1468	T05672	2	hypothetical prote
219	78	4.4	257	A97121	2	undecaprenyl pyrop
220	78	4.4	272	I48268	2	biliary glycoprote
221	78	4.4	286	A28333	2	carcinoembryonic a
222	78	4.4	335	C54312	2	pregnancy-specific
223	78	4.4	402	T09062	2	probable advanced
224	78	4.4	490	T43184	2	DEAD box ATP-depen
225	78	4.4	604	T41249	2	DEAD box ATP-depen
226	78	4.4	608	AB3562	2	gtp-binding protei
227	78	4.4	609	HMN2KA	1	hemagglutinin - ri
228	78	4.4	761	IJHUNG	1	neural cell adhesi
229	78	4.4	836	T42323	2	hypothetical prote
230	78	4.4	905	S43064	2	cadherin - African
231	78	4.4	905	T38314	2	CD8 alpha-chain -
232	77.5	4.4	172	T34227	2	exodeoxyribonuclea
233	77.5	4.4	214	C89833	2	SHP substrate-1 pr
234	77.5	4.4	236	T41012	2	SHP substrate-1 pr
235	77.5	4.4	239	I46082	2	F12G12.2 protein -
236	77.5	4.4	448	H98007	2	gluconate dehydrog
237	77.5	4.4	509	JC5288	2	ferrienterobactin-
238	77.5	4.4	513	JC5289	2	ferrienterobactin-
239	77.5	4.4	539	G86465	2	vascular cell adhe
240	77.5	4.4	591	H83362	2	dynamin-related pr
241	77.5	4.4	717	AD3097	2	neuraxin - rat
242	77.5	4.4	739	E98189	2	env protein - huma
243	77.5	4.4	757	A41288	1	hypothetical prote
244	77.5	4.4	863	S64742	2	polynucleotide pho
245	77.5	4.4	881	S06017	2	
246	77.5	4.4	968	S03068	2	
247	77.5	4.4	968	T25667	2	
248	77.5	4.4	991	T48631	2	

No.	%	Val	Description	Accession	Len	n
249	77.5	4.4	hypothetical prote	T32186	1015	2
250	77.5	4.4	hypothetical prote	T18713	1099	2
251	77.5	4.4	timeless protein T	T13759	1205	2
252	77.5	4.4	protein-tyrosine-p	B48758	1262	1
253	77.5	4.4	protein-tyrosine-p	A48758	1496	1
254	77.5	4.4	protein-tyrosine-p	C54689	1894	1
255	77.5	4.4	protein-tyrosine-p	A56178	1912	2
256	77.5	4.4	ubiquitin-protein	S12332	1950	2
257	77	4.3	Ig gamma-2 chain C	S06611	327	2
258	77	4.3	Ig gamma 1 chain c	I47158	328	2
259	77	4.3	50K glycoprotein p	JC5519	338	2
260	77	4.3	protein F2B2.6 [lim	B86353	398	2
261	77	4.3	probable membrane	S51378	439	2
262	77	4.3	voltage-gated pota	JE0276	491	2
263	77	4.3	SKS1 protein - yea	S61935	502	2
264	77	4.3	cytochrome P450 78	T05946	523	2
265	76.5	4.3	xylan 1,4-beta-xyl	JC7966	796	2
266	76.5	4.3	VLDL receptor prec	QRRBVD	873	1
267	76.5	4.3	leukocyte surface	I39207	1021	2
268	76.5	4.3	probable RND efflu	D83120	1029	2
269	76.5	4.3	probable membrane	S55862	1041	2
270	76.5	4.3	leukocyte antigen-	TDHULK	1897	1
271	76.5	4.3	cell wall-associat	AF1489	2167	2
272	76.5	4.3	herc2 protein - mo	T14346	4836	2
273	76.5	4.3	nonspecific cross-	C40428	177	2
274	76.5	4.3	molybdopterin-guan	E75132	191	1
275	76.5	4.3	hypothetical prote	T24314	238	2
276	76.5	4.3	hypothetical prote	S75312	251	2
277	76.5	4.3	conserved hypothet	G82131	296	2
278	76.5	4.3	hypothetical prote	D86291	390	2
279	76.5	4.3	hypothetical prote	S20905	394	2
280	76.5	4.3	pregnancy-specific	A54312	402	2
281	76.5	4.3	N-carbamyl-L-amino	AB1142	423	2
282	76.5	4.3	pregnancy-specific	C55181	426	2
283	76.5	4.3	pregnancy-specific	S09016	426	2
284	76.5	4.3	pregnancy-specific	B35334	426	2
285	76.5	4.3	pregnancy-specific	B55181	436	2
286	76.5	4.3	pregnancy-specific	A55181	495	2
287	76.5	4.3	yigC protein - Esc	D65189	497	2
288	76.5	4.3	DNA polymerase III	A71906	582	2
289	76.5	4.3	hypothetical prote	T23585	727	2
290	76.5	4.3	hypothetical prote	S17906	788	2
291	76.5	4.3	hypothetical prote	B96538	839	2
292	76.5	4.3	serine/threonine-s	D85350	876	2
293	76.5	4.3	Ig heavy chain - c	S71277	876	2
294	76.5	4.3	hypothetical prote	T18537	1005	2
295	76	4.3	suppressor protein	T19734	1043	2
296	76	4.3	platelet-derived g	T18307	1071	2
297	76	4.3	zinc finger protei	PFHUGA	1089	1
298	76	4.3	E-box-binding repr	JX0293	1124	2
299	76	4.3	ATP-dependent DNA	A56242	1154	2
300	76	4.3	probable polyketid	S62467	1328	2
301	76	4.3	HKR1 protein precu	B70588	1461	2
302	76	4.3	ankyrin-related un	S69703	1802	2
303	76	4.3	photosystem I prot	T15347	2039	2
304	76	4.3	mannose-specific p	S16199	138	2
305	76	4.3	Ig lambda chain -	AH1172	144	2
306	76	4.3	hypothetical prote	S49449	230	2
307	76	4.3	probable carboxype	T23147	239	2
308	76	4.3	probable carboxype	A64882	262	2
309	76	4.3	probable carboxype	H85751	262	2
310	76	4.3	prephenate dehydro	A99867	262	2
311	76	4.3	conserved hypothet	B97010	286	2
312	76	4.3	amalgam protein pr	H69759	305	2
313	76	4.3	brevican precursor	A31923	333	2
314	76	4.3	DNA-directed DNA p	I46268	378	1
315	76	4.3	hypothetical prote	S55194	487	2
316	76	4.3	L-asparagine perme	T47021	507	2
317	76	4.3	hypothetical prote	AD0236	508	2
318	76	4.3	hypothetical prote	G90497	550	2
319	76	4.3	hypothetical prote	T15577	758	2
320	76	4.3	hypothetical prote	T01011	841	2
321	76	4.3	hypothetical prote	T15746	964	2

Description	Accession	Len	n	Val	%	No.
macrophage colony-	S16385	978	2	4.3	76	322
neural adhesion pr	JC4211	1018	2	4.3	76	323
valine-tRNA ligase	T51503	1093	2	4.3	76	324
protein-tyrosine-p	TDFFLK	2029	1	4.3	76	325
myelin/oligodendro	A47712	246	2	4.3	75.5	326
pregnancy-specific	JC4124	326	2	4.3	75.5	327
T48 protein - frui	S42989	419	2	4.3	75.5	328
G beta repeat prot	T40614	421	2	4.3	75.5	329
hypothetical prote	T30130	432	2	4.3	75.5	330
exodeoxyribonuclea	A95140	446	2	4.3	75.5	331
chloroplast membra	A84689	462	2	4.3	75.5	332
hypothetical prote	T28076	485	2	4.3	75.5	333
hypothetical prote	T05744	819	2	4.3	75.5	334
neuronal cell surf	H69045	933	2	4.3	75.5	335
aggrecan precursor	S05944	1020	2	4.3	75.5	336
hypothetical prote	I50421	2109	1	4.3	75.5	337
probable anthranil	D95131	150	2	4.2	75	338
probable beta-keto	D71529	208	2	4.2	75	339
glucose-6-phosphat	D84906	466	2	4.2	75	340
glucose-6-phosphat	AC2650	491	2	4.2	75	341
glutamate/aspartat	B97432	503	2	4.2	75	342
Ig Y heavy chain (	S26609	543	2	4.2	75	343
Ig mu chain precur	B46529	572	2	4.2	75	344
hypothetical prote	S12838	573	2	4.2	75	345
microtubule-associ	B96751	622	2	4.2	75	346
ferrichrome-iron r	A55665	686	2	4.2	75	347
outer membrane rec	QRECFE	747	1	4.2	75	348
outer membrane rec	B85499	747	2	4.2	75	349
fibroblast growth	B90648	747	2	4.2	75	350
macrophage colony-	TVMSBK	821	1	4.2	75	351
neural cell adhesi	TVMSMD	976	1	4.2	75	352
CDO protein - rat	IJCHNL	1091	2	4.2	75	353
hypothetical prote	T03096	1256	2	4.2	75	354
elastic titin - hu	TO2206	1338	2	4.2	75	355
ovalbumin-related	I38346	7962	2	4.2	75	356
carcinoembryonic a	DXCH	232	1	4.2	74.5	357
hypothetical prote	A39037	278	2	4.2	74.5	358
hypothetical prote	T31908	309	2	4.2	74.5	359
probable lipoprote	S10006	321	2	4.2	74.5	360
lipoprotein [impor	D91078	379	2	4.2	74.5	361
lipoprotein D prec	E85923	379	2	4.2	74.5	362
hypothetical prote	B55522	379	2	4.2	74.5	363
conserved hypothet	T14884	463	2	4.2	74.5	364
conserved hypothet	D69539	518	2	4.2	74.5	365
protein-tyrosine k	I51593	544	2	4.2	74.5	366
triacylglycerol li	A47705	688	2	4.2	74.5	367
fibroblast growth	S51635	705	2	4.2	74.5	368
probable transport	F90739	741	2	4.2	74.5	369
probable transport	H85589	741	2	4.2	74.5	370
irregular chiasm C	A49448	764	2	4.2	74.5	371
hypothetical prote	T34376	771	2	4.2	74.5	372
probable membrane	H64817	786	2	4.2	74.5	373
hypothetical prote	T20609	795	2	4.2	74.5	374
env polyprotein -	VCLJG5	889	1	4.2	74.5	375
hypothetical prote	T00326	984	2	4.2	74.5	376
glutamate receptor	T19638	1003	2	4.2	74.5	377
glutamate receptor	PN0156	1007	2	4.2	74.5	378
contactin precurso	S28858	1008	2	4.2	74.5	379
[beta] subunit of	A57112	1021	2	4.2	74.5	380
DNA-directed RNA p	E87145	1178	2	4.2	74.5	381
brain-specific ang	S31145	1179	2	4.2	74.5	382
receptor DEC-205 -	T00028	1522	2	4.2	74.5	383
Down syndrome cell	S58880	1723	2	4.2	74.5	384
large repetitive p	T08851	1896	2	4.2	74.5	385
microtubule-associ	AD1018	2256	2	4.2	74.5	386
hypothetical prote	A56577	2364	2	4.2	74.5	387
T-cell receptor ga	T34416	2783	2	4.2	74.5	388
Ig kappa chain pre	S36291	203	2	4.2	74	389
biliary glycoprote	S01320	234	2	4.2	74	390
Ig gamma-2b chain	JC1506	234	2	4.2	74	391
hypothetical prote	PS0018	278	2	4.2	74	392
hypothetical prote	T19637	333	2	4.2	74	393
protein-glutamine	S68092	349	2	4.2	74	394

#	%	Score	Pos	Accession	Ct	Description
395	74	4.2	384	H64161	2	hypothetical prote
396	74	4.2	403	I52590	2	m33-B isoform - mo
397	74	4.2	424	T43498	2	hypothetical prote
398	74	4.2	463	C69997	2	probable proline t
399	74	4.2	468	S70297	2	SPS2 protein homol
400	74	4.2	502	T40792	2	hypothetical prote
401	74	4.2	548	A44302	2	protein-glutamine
402	74	4.2	586	T15259	2	hypothetical prote
403	74	4.2	611	F82442	2	probable peptide A
404	74	4.2	645	T39614	2	kinase-binding pro
405	74	4.2	673	T48701	2	hypothetical prote
406	74	4.2	860	JC5702	2	ErbB kinase activa
407	74	4.2	862	I49583	2	differentiation an
408	74	4.2	876	B96693	2	probable receptor
409	74	4.2	900	G96617	2	probable disease r
410	74	4.2	1063	A33830	2	cation efflux syst
411	74	4.2	1063	JC4700	2	cadmium, zinc, cob
412	74	4.2	1130	T23104	2	hypothetical prote
413	74	4.2	1133	T23103	2	hypothetical prote
414	74	4.2	1165	S45879	1	chitin synthase (E
415	73.5	4.2	1237	E86457	2	probable RNA helic
416	73.5	4.2	1367	T33819	2	hypothetical prote
417	73.5	4.2	1582	T15308	2	hypothetical prote
418	73.5	4.2	4344	A53489	2	dynein heavy chain
419	73.5	4.2	5232	A45086	2	HC-toxin synthetas
420	73.5	4.2	6658	T13931	2	projectin - fruit
421	73.5	4.2	325	S49451	2	cysteine proteinas
422	73.5	4.2	364	A30521	2	myeloid cell surfa
423	73.5	4.2	428	B83967	2	dihydroorotase pyr
424	73.5	4.2	647	T33773	2	hypothetical prote
425	73.5	4.2	740	AH0600	2	probable membrane
426	73.5	4.2	797	T27518	2	hypothetical prote
427	73.5	4.2	850	JC5700	2	ErbB kinase activa
428	73.5	4.1	880	VCLJS2	1	env polyprotein pr
429	73.5	4.1	923	F84732	2	probable ligand-ga
430	73.5	4.1	926	D83888	2	glucan 1,4-beta-gl
431	73.5	4.1	957	C69463	2	type I restriction
432	73.5	4.1	1166	S37692	2	probable tumor sup
433	73.5	4.1	1225	T48251	2	ubiquitin-protein
434	73.5	4.1	1240	T03097	2	CDO protein - huma
435	73.5	4.1	2013	AD1129	2	probable peptidogl
436	73.5	4.1	2042	T18399	2	variant-specific s
437	73.5	4.1	2301	GNNYTN	1	genome polyprotein
438	73.5	4.1	3255	G81702	2	adherence factor T
439	73.5	4.1	4544	S02392	2	alpha-2-macroglobu
440	73	4.1	147	T34265	1	hypothetical prote
441	73	4.1	220	G69047	2	conserved hypothet
442	73	4.1	235	S14675	2	Ig lambda chain -
443	73	4.1	250	S27544	2	hypothetical prote
444	73	4.1	293	H96906	2	hypothetical prote
445	73	4.1	322	H84095	2	hypothetical prote
446	73	4.1	354	T27712	2	hypothetical prote
447	73	4.1	389	T46722	2	conserved hypothet
448	73	4.1	397	E86304	2	F6I1.9 protein - A
449	73	4.1	413	S65948	2	hemolin - cecropia
450	73	4.1	413	A37778	1	hemolin precursor
451	73	4.1	432	RWMQT4	1	T-cell surface gly
452	73	4.1	476	H84524	2	probable fatty aci
453	73	4.1	519	S38921	2	hypothetical prote
454	73	4.1	590	I56526	1	interleukin 1 rece
455	73	4.1	666	A36026	2	kinesin-related pr
456	73	4.1	730	S64998	1	hypothetical prote
457	73	4.1	735	T00850	2	probable receptor-
458	73	4.1	853	IJBONC	2	neural cell adhesi
459	73	4.1	864	JH0438	2	penicillin-binding
460	73	4.1	901	P3XR17	2	core protein VP3 -
461	73	4.1	1014	T13476	2	hypothetical prote
462	73	4.1	1072	A38457	2	integrin alpha-6 c
463	73	4.1	1171	T31635	2	hypothetical prote
464	73	4.1	1179	T05673	2	hypothetical prote
465	73	4.1	1515	S51863	1	cadmium resistance
466	73	4.1	1737	A59235	2	unconventional myo
467	73	4.1	1806	T23298	2	probable membrane
468	73	4.1	3788	T30851	2	lysosomal traffick
469	72.5	4.1	202	S36293	2	T-cell receptor ga
470	72.5	4.1	221	T31620	2	hypothetical prote
471	72.5	4.1	334	G01650	2	malate dehydrogena
472	72.5	4.1	336	C27658	2	pregnancy-specific
473	72.5	4.1	342	AG1729	2	protein gp19 (Bact
474	72.5	4.1	351	B34595	2	pregnancy-specific
475	72.5	4.1	363	I39726	2	mannopine biosynth
476	72.5	4.1	371	T40287	2	hypothetical prote
477	72.5	4.1	377	B90437	2	hypothetical prote
478	72.5	4.1	399	AI1114	2	surface protein (p
479	72.5	4.1	424	A34595	2	pregnancy-specific
480	72.5	4.1	435	D33258	2	pregnancy-specific
481	72.5	4.1	440	S52895	2	TyA protein - yeas
482	72.5	4.1	443	AE3294	2	tolB protein [impo
483	72.5	4.1	478	A49228	2	trypsin-like prote
484	72.5	4.1	487	AI1146	2	hypothetical cell
485	72.5	4.1	491	T22844	2	hypothetical prote
486	72.5	4.1	527	D75127	2	hypothetical prote
487	72.5	4.1	666	A39610	2	SLY1 protein - yea
488	72.5	4.1	682	A35969	2	heparin-binding gr
489	72.5	4.1	687	T39838	2	hypothetical prote
490	72.5	4.1	768	JC7352	2	glucose-regulated
491	72.5	4.1	769	T45854	2	hypothetical prote
492	72.5	4.1	842	E96641	2	hypothetical prote
493	72.5	4.1	851	S44890	2	ncl-1 ZK12.2 prot
494	72.5	4.1	876	A49508	2	protein-tyrosine k
495	72.5	4.1	895	T11979	2	Preprotein translo
496	72.5	4.1	913	A48280	2	receptor tyrosine
497	72.5	4.1	1057	S45801	2	probable membrane
498	72.5	4.1	1123	AB0125	2	exodeoxyribonuclea
499	72.5	4.1	1138	A82939	2	membrane nuclease
500	72.5	4.1	1272	S26180	2	neurofascin - chic
501	72.5	4.1	1434	T30172	2	transmembrane prot
502	72.5	4.1	1575	T18545	2	lysobactin synthet
503	72.5	4.1	4367	B54802	1	dynein heavy chain
504	72.5	4.1	4924	T50176	2	probable peptide s
505	72.5	4.1	4936	AH2515	2	hypothetical prote
506	72	4.1	265	H72233	2	purine nucleoside
507	72	4.1	320	C89867	2	hypothetical prote
508	72	4.1	378	T51237	2	scarecrow-like pro
509	72	4.1	423	T29549	2	hypothetical prote
510	72	4.1	437	AF3613	2	hypothetical prote
511	72	4.1	442	E71523	2	hypothetical prote
512	72	4.1	446	B89922	2	conserved hypothet
513	72	4.1	469	C69628	2	gamma-aminobutyrat
514	72	4.1	506	F69867	2	two-component sens
515	72	4.1	510	A84707	2	probable pseudouri
516	72	4.1	521	E82377	2	ABC transporter, p
517	72	4.1	543	S38353	2	glutamate transpor
518	72	4.1	549	T33517	2	hypothetical prote
519	72	4.1	558	T01343	2	hypothetical prote
520	72	4.1	565	C82280	2	sensor kinase citA
521	72	4.1	585	S48929	2	hypothetical prote
522	72	4.1	599	T16774	2	hypothetical prote
523	72	4.1	617	T23197	2	hypothetical prote
524	72	4.1	646	I38049	2	cell surface glyco
525	72	4.1	783	T45899	2	receptor protein k
526	72	4.1	808	F81180	2	conserved hypothet
527	72	4.1	868	JC5701	2	ErbB kinase activa
528	72	4.1	873	H96503	2	protein F9C16.17 [
529	72	4.1	885	D86151	2	F22M8.8 protein -
530	72	4.1	900	T04839	2	protein kinase -
531	72	4.1	901	S07419	2	core protein P3 -
532	72	4.1	911	B34721	2	androgen receptor
533	72	4.1	1038	H90053	2	hypothetical prote
534	72	4.1	1186	T19334	2	hypothetical proce
535	72	4.1	1214	JC7259	2	Smad interacting p
536	72	4.1	1216	H85023	2	hypothetical prote
537	72	4.1	1273	T42405	2	sax-3 protein - Ca
538	72	4.1	1348	S51656	2	vascular endotheli
539	72	4.1	1906	S68235	1	myosin-light-chain
540	72	4.1	2383	D64962	2	probable membrane

Seq	Score	Val	Len	Accession	Description
541	72	4.1	4872	S27272	ryanodine receptor
542	71.5	4.0	145	S25743	Ig lambda chain -
543	71.5	4.0	229	B43685	nonstructural prot
544	71.5	4.0	238	A49633	Ig lambda-like cha
545	71.5	4.0	299	S50803	hypothetical prote
546	71.5	4.0	312	A64461	hypothetical prote
547	71.5	4.0	338	A64303	conserved hypothet
548	71.5	4.0	339	S08981	malate dehydrogena
549	71.5	4.0	362	T05167	hypothetical prote
550	71.5	4.0	443	T14916	mitosis-specific c
551	71.5	4.0	498	G90067	malate quinone oxi
552	71.5	4.0	500	T11946	ribosomal protein
553	71.5	4.0	542	AF2587	MFS permease [limpo
554	71.5	4.0	542	F97369	hypothetical prote
555	71.5	4.0	589	T50385	hypothetical coile
556	71.5	4.0	603	H84442	hypothetical prote
557	71.5	4.0	669	T48466	hypothetical prote
558	71.5	4.0	707	A38429	keratinocyte growt
559	71.5	4.0	707	A54846	fibroblast growth
560	71.5	4.0	764	QRHUGS	secretory componen
561	71.5	4.0	822	B54846	fibroblast growth
562	71.5	4.0	919	S33942	hexon protein - hu
563	71.5	4.0	921	F71486	probable yopC/gen
564	71.5	4.0	1032	H64100	acriflavine resist
565	71.5	4.0	1089	S33727	platelet-derived g
566	71.5	4.0	1180	E86719	hypothetical prote
567	71.5	4.0	1348	S27812	probable epidermal
568	71.5	4.0	1348	A43917	probable epidermal
569	71.5	4.0	1374	S62524	probable RNA helic
570	71.5	4.0	1377	C70148	DNA-directed RNA p
571	71.5	4.0	1413	D84481	probable retroelem
572	71.5	4.0	1462	T11648	probable mitotic s
573	71.5	4.0	2397	A55535	versican precursor
574	71	4.0	61	C82536	hypothetical prote
575	71	4.0	142	S38392	T-cell receptor be
576	71	4.0	189	G64496	hypothetical prote
577	71	4.0	207	T50206	hypothetical zinc
578	71	4.0	221	T21117	hypothetical prote
579	71	4.0	224	H81568	conserved hypothet
580	71	4.0	231	B86520	CT181 hypothetical
581	71	4.0	231	G72102	ct181 hypothetical
582	71	4.0	258	T27033	MG256 homolog H91_
583	71	4.0	329	DEDFLM	L-lactate dehydrog
584	71	4.0	333	AF0407	lipoprotein [limpo
585	71	4.0	343	AI0358	probable fimbrial
586	71	4.0	344	I56551	neurocrimin - rat
587	71	4.0	345	I48780	Stral/Eplg2 protei
588	71	4.0	346	AF1820	sialoglycoproteina
589	71	4.0	387	B71611	hypothetical prote
590	71	4.0	389	S68155	ubiquinol-cytochro
591	71	4.0	390	T27033	hypothetical prote
592	71	4.0	407	T34442	hypothetical prote
593	71	4.0	423	EHMSS	Ig epsilon chain C
594	71	4.0	455	S50391	drought-inducible
595	71	4.0	462	JN0719	amino acid transpo
596	71	4.0	463	AH1758	M9-R protein - myx
597	71	4.0	509	WMVZMX	probable pyruvate
598	71	4.0	570	T11647	GTP-binding protei
599	71	4.0	609	H82039	gluconate 2-dehydr
600	71	4.0	615	B38575	hypothetical prote
601	71	4.0	682	T22064	soluble vascular e
602	71	4.0	687	A49636	triacylglycerol li
603	71	4.0	690	A24545	glycerol ester hyd
604	71	4.0	691	B89797	hypothetical prote
605	71	4.0	765	E96558	fibroblast growth
606	71	4.0	821	TVHUF2	WD40-repeat protei
607	71	4.0	876	T51507	probable carrier p
608	71	4.0	902	S54495	hypothetical prote
609	71	4.0	940	T41992	isoleucine-tRNA li
610	71	4.0	956	G70327	contactin 1 precur
611	71	4.0	1018	A54744	receptor protein k
612	71	4.0	1027	B85089	regulatory protein
613	71	4.0	1082	S64903	hypothetical prote
614	71	4.0	1217	T22672	hypothetical prote
615	71	4.0	1251	T21189	hypothetical prote
616	71	4.0	1338	S09982	protein-tyrosine k
617	71	4.0	4391	A38096	perlecan precursor
618	71	4.0	5107	T29144	partial CDS - Caen
619	70.5	4.0	203	F69381	flagellin (flaB1-1
620	70.5	4.0	223	A81068	hypothetical prote
621	70.5	4.0	238	D86302	hypothetical prote
622	70.5	4.0	246	B82764	hypothetical prote
623	70.5	4.0	332	T45770	hypothetical prote
624	70.5	4.0	338	DERTMM	malate dehydrogena
625	70.5	4.0	358	B41902	protein R09F10.8 [
626	70.5	4.0	429	G01923	arsenical pump mem
627	70.5	4.0	455	T19108	KIR (cl-5) NK rece
628	70.5	4.0	502	T15159	hypothetical prote
629	70.5	4.0	505	T26319	hypothetical prote
630	70.5	4.0	522	TVFV60	hypothetical prote
631	70.5	4.0	526	TVCHS	protein-tyrosine k
632	70.5	4.0	533	A45501	protein-tyrosine k
633	70.5	4.0	537	S52313	protein-tyrosine k
634	70.5	4.0	545	S52314	protein-tyrosine k
635	70.5	4.0	546	TVFVS2	protein-tyrosine k
636	70.5	4.0	557	MWXRRT	protein-tyrosine k
637	70.5	4.0	558	TVFVS1	RNA 10 protein - r
638	70.5	4.0	568	A45624	protein-tyrosine k
639	70.5	4.0	569	TVFVPR	trophozoite cystei
640	70.5	4.0	587	S14683	protein-tyrosine k
641	70.5	4.0	627	A69663	Ig mu chain precur
642	70.5	4.0	630	A39344	DNA mismatch repai
643	70.5	4.0	646	T48644	tumor-associated m
644	70.5	4.0	656	H84206	negative regulator
645	70.5	4.0	663	TVMVRR	acetyl-CoA synthet
646	70.5	4.0	669	T13640	protein-tyrosine k
647	70.5	4.0	743	F71062	probable minor str
648	70.5	4.0	787	T41974	hypothetical prote
649	70.5	4.0	793	T41703	replication origin
650	70.5	4.0	844	S05988	dipeptidyl aminope
651	70.5	4.0	877	IJBOCN	translation elonga
652	70.5	4.0	878	S11842	N-cadherin precurs
653	70.5	4.0	895	A55413	hypothetical prote
654	70.5	4.0	906	IJMSCN	triglyceride trans
655	70.5	4.0	928	G86546	N-cadherin precurs
656	70.5	4.0	928	G81591	polymorphic outer
657	70.5	4.0	938	F86548	polymorphic membra
658	70.5	4.0	938	H72074	polymorphic outer
659	70.5	4.0	1088	B56715	polymorphic membra
660	70.5	4.0	1200	T17404	calcium receptor (
661	70.5	4.0	1356	JC1402	hyalin - sea urchi
662	70.5	4.0	1402	F84480	protein-tyrosine k
663	70.5	4.0	1427	I51669	probable retroelem
664	70.5	4.0	1694	S50065	tumor suppressor -
665	70.5	4.0	2051	T30938	sialoadhesin - mou
666	70.5	4.0	2303	GNNYTP	receptor tyrosine
667	70.5	4.0	2303	S13554	genome polyprotein
668	70.5	4.0	2464	QRMSP1	genome polyprotein
669	70.5	4.0	6831	A88852	microtubule-associ
670	70.5	4.0	6839	S57242	protein unc-22 [lim
671	70.5	4.0	7160	T27935	twitchin (similari
672	70.5	4.0	115	KVMSL6	hypothetical prote
673	70	4.0	203	S23043	Ig kappa chain pre
674	70	4.0	224	I37243	T-cell receptor ga
675	70	4.0	236	S25746	CMRF-35 antigen -
676	70	4.0	283	AB0105	Ig lambda chain -
677	70	4.0	292	T44230	probable maltodext
678	70	4.0	299	D83010	hypothetical prote
679	70	4.0	304	G71624	probable binding p
680	70	4.0	347	T29415	rifin PFB0025c - m
681	70	4.0	356	G82938	hypothetical prote
682	70	4.0	374	A46352	hypothetical prote
683	70	4.0	403	B36151	hemin, transport sy
684	70	4.0	410	IS0494	ORF1 protein - Chl
685	70	4.0	469	T45929	tryptophan synthas
686	70	4.0			serine proteinase

Seq	%	Score	Length	N	Accession	Description
687	70	4.0	491	2	T27661	hypothetical prote
688	70	4.0	517	2	T00980	hypothetical prote
689	70	4.0	536	2	T37544	hypothetical serin
690	70	4.0	548	2	B71549	hypothetical serin
691	70	4.0	550	2	T03714	5-epi-aristolochen
692	70	4.0	576	2	A32604	interleukin-1 rece
693	70	4.0	599	2	T48450	hypothetical prote
694	70	4.0	609	2	AE2062	gamma-glutamyltran
695	70	4.0	611	1	WIWLEP	E1 protein - Europ
696	70	4.0	611	2	H70938	probable fadE5 pro
697	70	4.0	648	2	T08856	hypothetical prote
698	70	4.0	687	2	A39045	protein-glutamine
699	70	4.0	790	2	T01537	S-receptor kinase
700	70	4.0	805	2	S68441	leptin receptor, s
701	70	4.0	810	1	S57196	calpain (EC 3.4.22
702	70	4.0	818	2	T32154	hypothetical prote
703	70	4.0	828	2	AD2004	hypothetical prote
704	70	4.0	837	2	A34898	granulocyte colony
705	70	4.0	838	2	AC1064	outer membrane fim
706	70	4.0	849	2	T22306	hypothetical prote
707	70	4.0	892	2	S68439	leptin receptor, s
708	70	4.0	894	2	S68437	leptin receptor, s
709	70	4.0	900	2	S68440	leptin receptor, s
710	70	4.0	933	2	H90247	ATP-dependent heli
711	70	4.0	990	2	T16554	hypothetical prote
712	70	4.0	1040	2	A34695	axonal glycoprotei
713	70	4.0	1086	2	T40354	hypothetical prote
714	70	4.0	1092	2	T30214	fibrinogen-binding
715	70	4.0	1162	2	S68438	leptin receptor, s
716	70	4.0	1190	2	T00842	probable histidine
717	70	4.0	1317	2	B41950	retrovirus-related
718	70	4.0	1456	1	WMWGPV	RNA-directed RNA p
719	70	4.0	1456	2	JQ2294	hypothetical prote
720	70	4.0	2004	2	AC0314	probable membrane
721	70	4.0	2183	2	T42764	coagulation factor
722	70	4.0	4199	2	S76412	hypothetical prote
723	69.5	3.9	285	2	S74483	hypothetical prote
724	69.5	3.9	332	1	I38548	alcohol sulfotrans
725	69.5	3.9	338	1	DEMSMM	malate dehydrogena
726	69.5	3.9	346	2	T49148	nitrilase (EC 3.5.
727	69.5	3.9	366	2	E97304	iron-regulated ABC
728	69.5	3.9	407	2	T08732	hypothetical prote
729	69.5	3.9	427	2	C23703	ribulose-bisphosph
730	69.5	3.9	437	2	D70353	adenylosuccinate l
731	69.5	3.9	442	2	H86144	hypothetical prote
732	69.5	3.9	444	2	F97750	tolB protein precu
733	69.5	3.9	447	2	B81519	UDP-N-acetylmuramo
734	69.5	3.9	447	2	A86603	muramoyl-DAP ligas
735	69.5	3.9	447	2	F72021	muramoyl-dap ligas
736	69.5	3.9	453	2	B88040	protein lin-42 (im
737	69.5	3.9	461	2	T47782	hypothetical prote
738	69.5	3.9	503	2	S63257	probable membrane
739	69.5	3.9	506	2	T05272	fatty acid elongas
740	69.5	3.9	523	1	TVFVMT	protein-tyrosine k
741	69.5	3.9	548	1	A26511	amdS protein - Eme
742	69.5	3.9	548	2	S27958	transcription fact
743	69.5	3.9	568	2	T39840	conserved hypothet
744	69.5	3.9	568	2	A39395	delayed rectifier
745	69.5	3.9	585	2	D64569	conserved hypothet
746	69.5	3.9	616	2	S19352	amino acid transpo
747	69.5	3.9	633	2	T43724	dnaK-type molecula
748	69.5	3.9	640	2	D90946	hypothetical prote
749	69.5	3.9	682	2	H85794	probable membrane
750	69.5	3.9	682	2	A41798	hypothetical prote
751	69.5	3.9	710	1	I51283	carboxy-terminal p
752	69.5	3.9	736	2	T40904	hepatocyte growth
753	69.5	3.9	757	2	T24266	pombe specific hyp
754	69.5	3.9	776	2	A41704	hypothetical prote
755	69.5	3.9	776	2	F81289	genome polyprotein
756	69.5	3.9	846	2	T04533	probable sugar tra
757	69.5	3.9	849	1	UYPVAD	hypothetical prote
758	69.5	3.9	1034	2	H86399	noncapsid protein
759	69.5	3.9	1045	2	G69167	protein F17L21.26

Seq	%	Score	Length	N	Accession	Description
760	69.5	3.9	1045	2	G69167	cobalamin biosynth
761	69.5	3.9	1102	2	T28666	protein kinase C-r
762	69.5	3.9	1172	2	F70535	probable rpoB prot
763	69.5	3.9	1199	2	C71500	probable swi/snf h
764	69.5	3.9	1260	1	S05479	neural cell adhesi
765	69.5	3.9	1463	2	T30290	AAS surface protei
766	69.5	3.9	1832	2	AC2594	glutamate synthase
767	69.5	3.9	1858	2	D97376	hypothetical prote
768	69	3.9	115	2	C90907	hypothetical prote
769	69	3.9	139	2	AH1847	photosystem I reac
770	69	3.9	222	2	A69458	conserved hypothet
771	69	3.9	279	2	S04693	T-cell receptor de
772	69	3.9	289	2	T18048	hypothetical prote
773	69	3.9	291	2	A87153	carbohydrate degra
774	69	3.9	306	2	T25625	hypothetical prote
775	69	3.9	330	2	AD1533	hypothetical prote
776	69	3.9	348	2	D96815	probable gamma-glu
777	69	3.9	363	2	AG0675	probable secreted
778	69	3.9	390	2	F72863	AcOrf-109 protein
779	69	3.9	391	2	T41849	AcMNPV orf109 - Bo
780	69	3.9	396	2	T36678	probable septum si
781	69	3.9	418	2	T35753	probable periplasm
782	69	3.9	428	2	S09134	gene ND4L intron 1
783	69	3.9	461	2	F83772	SERINE CARBOXYPEPT
784	69	3.9	465	2	B85358	hypothetical prote
785	69	3.9	469	2	T46930	cytochrome P450 2C
786	69	3.9	490	2	B28516	L1 protein - bovin
787	69	3.9	493	2	E71008	hypothetical prote
788	69	3.9	501	1	P1WLB2	L1 protein - bovin
789	69	3.9	505	1	PWYCA	leptin receptor, s
790	69	3.9	542	2	T20457	hypothetical prote
791	69	3.9	584	1	ALBY	alpha-glucosidase
792	69	3.9	615	2	JE0358	ralB binding prote
793	69	3.9	633	2	D82527	proteinase IV XF26
794	69	3.9	644	2	A25684	hypothetical prote
795	69	3.9	653	2	A54366	sodium/phosphate c
796	69	3.9	657	2	S25184	csp1 protein - Cor
797	69	3.9	715	2	I45832	scinderin - bovine
798	69	3.9	715	2	T10049	adseverin - mouse
799	69	3.9	773	2	T46283	hypothetical prote
800	69	3.9	824	2	T51057	related to tol pro
801	69	3.9	919	2	C86578	YopC/Gen secretion
802	69	3.9	919	2	F72045	type III secretion
803	69	3.9	1049	2	S67613	vacuolar carboxype
804	69	3.9	1052	2	A82127	ribonuclease E VC2
805	69	3.9	1244	2	T19615	hypothetical prote
806	69	3.9	1283	2	T39174	hypothetical Serin
807	69	3.9	1357	2	S61187	hypothetical prote
808	69	3.9	1360	2	T32833	probable membrane
809	69	3.9	1442	2	T18538	hypothetical prote
810	69	3.9	1656	2	S54520	patched protein -
811	69	3.9	1802	2	S52611	probable membrane
812	69	3.9	2132	2	A55182	TyB protein - yeas
813	69	3.9	2437	1	T18482	aggrecan precursor
814	69	3.9	4563	1	LPHUB	hypothetical prote
815	69	3.9	5188	1	B85547	apolipoprotein B-1
816	69	3.9	5291	2	F90696	probable RTX famil
817	69	3.9	107797	2	T30192	hypothetical prote
818	68.5	3.9	134	2	S11245	probable peptide s
819	68.5	3.9	135	2	JQ0472	Ig kappa chain pre
820	68.5	3.9	145	2	S36324	T-cell receptor de
821	68.5	3.9	227	2	T33766	T-cell receptor be
822	68.5	3.9	228	2	AE2200	hypothetical prote
823	68.5	3.9	234	2	S25757	two-component resp
824	68.5	3.9	234	2	S14237	Ig lambda chain -
825	68.5	3.9	240	2	A39016	Ig kappa chain pre
826	68.5	3.9	267	2	G90579	T-cell surface gly
827	68.5	3.9	268	2	S48942	hypothetical prote
828	68.5	3.9	292	2	C64699	hypothetical prote
829	68.5	3.9	296	2	G65002	proteinase IV (EC
830	68.5	3.9	299	2	T32094	hypothetical prote
831	68.5	3.9	310	2	A41776	syndecan 1 precurs
832	68.5	3.9	327	2	A81192	replication protei

No.	Ident	Score	Len	N	Accession	Description
833	68.5	3.9	328	2	I47161	Ig gamma 3 chain c
834	68.5	3.9	329	2	T19872	hypothetical prote
835	68.5	3.9	366	2	A70852	hypothetical prote
836	68.5	3.9	375	2	E96567	hypothetical prote
837	68.5	3.9	393	2	B48965	subtilin biosynthe
838	68.5	3.9	423	2	AG0451	maltoporin [import
839	68.5	3.9	448	2	G69960	exodeoxyribonuclea
840	68.5	3.9	458	1	RWHUT4	T-cell surface gly
841	68.5	3.9	463	2	T19943	hypothetical prote
842	68.5	3.9	464	2	T06176	ribulose-bisphosph
843	68.5	3.9	493	2	T41397	DNA damage inducib
844	68.5	3.9	498	2	JQ2353	glycoprotein E pre
845	68.5	3.9	513	2	H90401	flagella-related p
846	68.5	3.9	542	2	S30084	SRP1 protein - yea
847	68.5	3.9	555	2	F70372	dihydroxyacid dehy
848	68.5	3.9	561	2	S63388	probable membrane
849	68.5	3.9	561	2	A59182	protein-tyrosine k
850	68.5	3.9	581	2	C71078	aldehyde-ferredoxi
851	68.5	3.9	589	2	T40252	hypothetical prote
852	68.5	3.9	592	2	S54489	phosphoribosylamin
853	68.5	3.9	601	2	AD1250	DNA mismatch repai
854	68.5	3.9	606	2	AF2903	GTP-binding tyrosi
855	68.5	3.9	606	2	H97678	hypothetical prote
856	68.5	3.9	630	2	S77346	hypothetical prote
857	68.5	3.9	636	2	A86248	protein T23J18.9 [
858	68.5	3.9	654	2	A69656	methyl-accepting c
859	68.5	3.9	672	2	D81746	type III secretion
860	68.5	3.9	689	2	S70661	transferrin-bindin
861	68.5	3.9	772	2	T05753	s-receptor kinase
862	68.5	3.9	776	2	B41704	genome polyprotein
863	68.5	3.9	789	2	S62172	SHE4 protein - yea
864	68.5	3.9	818	2	B83537	hypothetical prote
865	68.5	3.9	827	2	A37849	S-layer protein -
866	68.5	3.9	831	2	JQ1655	prolactin receptor
867	68.5	3.9	906	1	IJHUCN	cadherin 2 precurs
868	68.5	3.9	950	2	T51134	ionotropic glutama
869	68.5	3.9	972	1	TVHUMD	macrophage colony-
870	68.5	3.9	976	2	A42466	alpha-amylase (EC
871	68.5	3.9	1043	2	A56037	DNA-binding protei
872	68.5	3.8	1074	2	F72217	conserved hypothet
873	68.5	3.8	1086	2	T18294	Ca2+-transporting
874	68.5	3.8	1134	2	S53955	hypothetical prote
875	68.5	3.8	1257	1	A41060	neural cell adhesi
876	68.5	3.8	1269	2	A90267	proteinase related
877	68.5	3.8	1466	2	A36426	SPA2 protein - yea
878	68.5	3.8	1520	2	A81731	polymorphic membra
879	68.5	3.8	1767	2	T20766	hypothetical prote
880	68.5	3.8	2013	2	AI1489	probable peptidogl
881	68.5	3.8	2288	2	T30568	acetyl-CoA carboxy
882	68.5	3.8	3229	2	S27852	probable cell-surf
883	68.5	3.8	4116	2	T13719	calo protein - fru
884	68	3.8	142	2	S36307	T-cell receptor de
885	68	3.8	144	2	AI1529	mannose-specific p
886	68	3.8	155	2	I64130	PAL cross-reacting
887	68	3.8	157	2	T09659	pathogenesis-relat
888	68	3.8	180	2	A71634	hypothetical prote
889	68	3.8	221	2	S73349	adhesin P1 precurs
890	68	3.8	231	2	D64461	hypothetical prote
891	68	3.8	233	2	H95345	NapC membrane prot
892	68	3.8	266	2	G69483	hypothetical prote
893	68	3.8	275	2	S03967	intercellular adhe
894	68	3.8	276	2	D82169	conserved hypothet
895	68	3.8	286	2	A82159	transmembrane sens
896	68	3.8	311	2	AH3197	protein farnesyltr
897	68	3.8	326	2	T51811	probable aliphatic
898	68	3.8	330	2	B96027	oligopeptide ABC t
899	68	3.8	338	2	C83653	farnesyltransferas
900	68	3.8	340	2	T49006	permease protein o
901	68	3.8	341	2	AE1824	synaptotagmin VIII
902	68	3.8	355	2	S58401	probable DNA polym
903	68	3.8	371	2	A71378	probable elongatio
904	68	3.8	378	2	E84806	hypothetical prote
905	68	3.8	385	2	T27626	hypothetical prote

No.	Ident	Score	Len	N	Accession	Description
906	68	3.8	401	2	B89863	argininosuccinate
907	68	3.8	409	1	PAWTF	fructose-bisphosph
908	68	3.8	412	2	T35564	probable prokaryot
909	68	3.8	431	2	F64072	probable oxidoredu
910	68	3.8	444	2	D87296	multidrug resistan
911	68	3.8	459	2	S76138	hypothetical prote
912	68	3.8	459	2	T21105	hypothetical prote
913	68	3.8	466	2	T46054	hypothetical prote
914	68	3.8	471	2	A81680	conserved hypothet
915	68	3.8	479	1	S22542	transcription fact
916	68	3.8	526	2	P5XR10	outer capsid prote
917	68	3.8	528	2	T38027	hypothetical prote
918	68	3.8	541	2	E96789	protein T23E18.10
919	68	3.8	584	2	S46183	alpha-glucosidase
920	68	3.8	602	2	D90557	hypothetical prote
921	68	3.8	632	2	T37810	RNA-binding post-t
922	68	3.8	637	2	D82816	fimbrial assembly
923	68	3.8	638	2	S54418	fibronectin-bindin
924	68	3.8	640	2	S35734	DNA topoisomerase
925	68	3.8	645	2	E96631	probable receptor
926	68	3.8	649	1	C2CLDM	cellulase (EC 3.2.
927	68	3.8	656	2	F71675	hypothetical prote
928	68	3.8	690	2	JC4185	proteinase II (EC
929	68	3.8	710	2	F82492	GGDEF family prote
930	68	3.8	721	2	T27570	hypothetical prote
931	68	3.8	789	2	S28259	androgen-regulated
932	68	3.8	793	2	D38992	cadherin 8 - human
933	68	3.8	795	2	T21487	hypothetical prote
934	68	3.8	796	2	T39962	coatomer complex b
935	68	3.8	814	2	C40618	fimbrial outer mem
936	68	3.8	878	2	AH2075	ferrichrome-iron r
937	68	3.8	896	2	S26984	probable DNA-direc
938	68	3.8	901	2	JE0062	core protein VP3 -
939	68	3.8	906	1	IJXLC2	N-cadherin 2 precu
940	68	3.8	912	2	A54423	brevican precursor
941	68	3.8	940	2	AB1744	internalin protein
942	68	3.8	962	2	S03818	carboxymethylcellu
943	68	3.8	963	2	A57238	iron-responsive el
944	68	3.8	997	2	D84473	protein F40H6.2 [i
945	68	3.8	1019	2	T13039	tyrosine kinase re
946	68	3.8	1071	2	T52306	methionine S-methy
947	68	3.8	1147	2	S64930	serine/threonine-s
948	68	3.8	1174	2	I38140	protein-tyrosine-p
949	68	3.8	1192	2	F88062	protein ZK250.10 [
950	68	3.8	1195	2	S61886	chitin synthase (E
951	68	3.8	1281	2	I48123	p-glycoprotein iso
952	68	3.8	1282	2	JC4393	microbial collagen
953	68	3.8	1291	2	T21694	hypothetical prote
954	68	3.8	1295	2	T30528	reverse transcript
955	68	3.8	1318	2	T05745	hypothetical prote
956	68	3.8	1458	2	A45665	adult-specific bru
957	68	3.8	1466	2	T32422	hypothetical prote
958	68	3.8	1664	2	H82601	conserved hypothet
959	68	3.8	1707	2	T18951	hypothetical prote
960	68	3.8	1786	2	H71527	probable excinucle
961	68	3.8	1946	2	AE1449	hypothetical prote
962	68	3.8	2124	2	A28452	hypothetical prote
963	68	3.8	3341	2	A42996	genome polyprotein
964	67.5	3.8	134	2	T14454	proteoglycan core
965	67.5	3.8	177	2	H90493	cytochrome b5 - wi
966	67.5	3.8	212	2	S03964	stem bromelain (EC
967	67.5	3.8	221	1	B42521	hypothetical prote
968	67.5	3.8	229	2	A20969	Ig kappa chain pre
969	67.5	3.8	261	2	S55199	hypothetical prote
970	67.5	3.8	267	2	I72882	Fc gamma receptor
971	67.5	3.8	278	2	E97703	hypothetical prote
972	67.5	3.8	278	2	JC1507	biliary glycoprote
973	67.5	3.8	299	2	F82975	hypothetical prote
974	67.5	3.8	315	2	G69785	hypothetical prote
975	67.5	3.8	327	2	T22407	hypothetical prote
976	67.5	3.8	329	1	G2GP	Ig gamma-2 chain C
977	67.5	3.8	345	1	I58406	LERK-2 - rat
978	67.5	3.8	348	1	MNNHPB	outer membrane pro

No.	Score		Len	Accession	Ct	Description
979	67.5	3.8	348	B70743	2	hypothetical prote
980	67.5	3.8	357	T34012	2	hypothetical prote
981	67.5	3.8	360	T27022	2	hypothetical prote
982	67.5	3.8	361	D83798	2	phosphoserine amin
983	67.5	3.8	362	AE1397	2	conserved hypothet
984	67.5	3.8	364	T46630	2	cysteine proteinas
985	67.5	3.8	364	T12039	2	cysteine proteinas
986	67.5	3.8	367	AF2494	2	hypothetical prote
987	67.5	3.8	370	S29139	2	aggrecan - pig (fr
988	67.5	3.8	402	T25732	2	hypothetical prote
989	67.5	3.8	426	I36948	2	Ig epsilon-chain -
990	67.5	3.8	443	T19512	2	hypothetical prote
991	67.5	3.8	450	H71135	2	probable adenylosu
992	67.5	3.8	451	T06090	2	hypothetical prote
993	67.5	3.8	458	A83095	2	UDP-N-acetylmuramo
994	67.5	3.8	466	AI1894	2	two-component sens
995	67.5	3.8	487	S65133	2	butyrophilin - mou
996	67.5	3.8	510	A87482	2	conserved hypothet
997	67.5	3.8	511	A46020	2	potassium channel
998	67.5	3.8	511	S07095	2	potassium channel
999	67.5	3.8	525	JQ0642	2	59K antigen - Chla
1000	67.5	3.8	527	G85760	2	hypothetical prote
1001	67.5	3.8	527	H90858	2	hypothetical prote
1002	67.5	3.8	541	A43610	2	protein-tyrosine k
1003	67.5	3.8	542	TVHUSC	1	protein-tyrosine k
1004	67.5	3.8	547	B45808	2	B-lymphocyte antig
1005	67.5	3.8	547	T27253	2	hypothetical prote
1006	67.5	3.8	567	S29498	2	lymphocyte antigen
1007	67.5	3.8	570	AI1828	2	flavoprotein [impo
1008	67.5	3.8	572	S55982	2	asparagine synthas
1009	67.5	3.8	584	S48327	2	hypothetical prote
1010	67.5	3.8	591	S73708	2	MG321 homolog H08_
1011	67.5	3.8	619	AI3336	2	potassium/proton a
1012	67.5	3.8	621	A72091	2	metalloproteinase
1013	67.5	3.8	621	D81578	2	zinc proteinase CP
1014	67.5	3.8	627	D96956	2	ntrC family transc
1015	67.5	3.8	651	T49986	2	lectin-like protei
1016	67.5	3.8	697	E95196	2	neuraminidase B [i
1017	67.5	3.8	726	AG0837	2	TonB-dependent out
1018	67.5	3.8	732	JU0132	1	acylaminoacyl-pept
1019	67.5	3.8	748	I48744	2	semaphorin A - mou
1020	67.5	3.8	759	S67164	2	probable membrane
1021	67.5	3.8	776	S67053	2	probable membrane
1022	67.5	3.8	790	G02678	2	cadherin-14 - huma
1023	67.5	3.8	790	A39627	2	protein-tyrosine k
1024	67.5	3.8	832	AD1096	2	internalin protein
1025	67.5	3.8	837	B89583	2	protein K07E3.2 [i
1026	67.5	3.8	855	T10665	2	hypothetical prote
1027	67.5	3.8	866	T10587	2	serine/threonine-s
1028	67.5	3.8	879	S73757	2	hypothetical prote
1029	67.5	3.8	906	AG1957	2	hypothetical prote
1030	67.5	3.8	926	D86897	2	hypothetical membr
1031	67.5	3.8	933	AD3309	2	chitin synthase (B
1032	67.5	3.8	944	T47246	2	glutamate ionotrop
1033	67.5	3.8	956	JH0826	2	Env protein - Maed
1034	67.5	3.8	992	JQ1165	2	evolved beta-D-gal
1035	67.5	3.8	1036	A29832	2	evolved beta-D-gal
1036	67.5	3.8	1042	E85968	2	conserved hypothet
1037	67.5	3.8	1042	F91123	2	hypothetical prote
1038	67.5	3.8	1061	D98008	2	probable pyrolysin
1039	67.5	3.8	1118	T27865	2	chitinase A [impor
1040	67.5	3.8	1155	H71456	2	P-glycoprotein-lik
1041	67.5	3.8	1215	T43916	2	P-glycoprotein-lik
1042	67.5	3.8	1229	D85023	2	protein-tyrosine k
1043	67.5	3.8	1229	T52319	2	hypothetical prote
1044	67.5	3.8	1260	TVRTNU	1	embryonic receptor
1045	67.5	3.8	1263	T13465	2	myosin-2 isoform -
1046	67.5	3.8	1330	S49010	2	beta-galactosidase
1047	67.5	3.8	1471	T40117	2	kinase-related pro
1048	67.5	3.8	1928	JS0610	2	variant surface pr
1049	67.5	3.8	2338	I73957	2	gp330 protein prec
1050	67.5	3.8	3026	T28431	2	
1051	67.5	3.8	4660	T42737	2	

No.	Score		Len	Accession	Ct	Description
1052	67	3.8	127	S52447	2	Ig kappa chain V r
1053	67	3.8	128	S31488	2	Ig kappa chain pre
1054	67	3.8	131	E30552	2	T-cell activation
1055	67	3.8	135	S49200	2	cytochrome b5 - co
1056	67	3.8	175	B70221	2	rev protein (rev)
1057	67	3.8	182	T23259	2	hypothetical prote
1058	67	3.8	214	B71169	2	probable flagellin
1059	67	3.8	239	AC2042	2	hypothetical prote
1060	67	3.8	255	F69962	2	amino acid ABC tra
1061	67	3.8	282	B84984	2	geranyltransferase
1062	67	3.8	300	H64050	2	glucose kinase hom
1063	67	3.8	302	AC1387	2	phosphate ABC tran
1064	67	3.8	302	AE1762	2	phosphate ABC tran
1065	67	3.8	311	C86638	2	glycosyl transfera
1066	67	3.8	358	G64461	2	biotin synthase (E
1067	67	3.8	373	PDBYB	1	REP1 protein - yea
1068	67	3.8	430	T14420	2	s-locus-specific g
1069	67	3.8	441	F71425	2	hypothetical prote
1070	67	3.8	450	S38424	2	s-locus-specific g
1071	67	3.8	461	T09933	2	probable phosphodi
1072	67	3.8	474	I50830	2	Ig mu chain - Lepi
1073	67	3.8	477	G86833	2	6-phospho-beta-glu
1074	67	3.8	495	A26396	2	T-cell surface gly
1075	67	3.8	518	JC4024	2	poliovirus recepto
1076	67	3.8	524	G64243	2	hypothetical prote
1077	67	3.8	532	C97228	2	probable peptide A
1078	67	3.8	542	T41650	2	importin alpha sub
1079	67	3.8	544	S41626	2	spike protein chai
1080	67	3.8	569	S64957	2	aspergillopepsin I
1081	67	3.8	599	S55363	2	maltase-like prote
1082	67	3.8	619	S67067	2	probable membrane
1083	67	3.8	622	H64447	2	hypothetical prote
1084	67	3.8	623	A64774	2	ybaU protein - Esc
1085	67	3.8	625	S52485	2	glucokinase regula
1086	67	3.8	661	G71063	1	probable ferrous i
1087	67	3.8	690	H71237	2	hypothetical prote
1088	67	3.8	717	T25431	2	hypothetical prote
1089	67	3.8	721	AI2447	2	hypothetical prote
1090	67	3.8	746	A75018	2	transport protein
1091	67	3.8	747	T23607	2	hypothetical prote
1092	67	3.8	750	T19080	2	hypothetical prote
1093	67	3.8	836	B84417	2	hypothetical prote
1094	67	3.8	850	AF3484	2	cell surface glyco
1095	67	3.8	852	A28459	2	hypothetical trans
1096	67	3.8	871	G86586	2	cell surface glyco
1097	67	3.8	871	D72038	2	DNA topoisomerase
1098	67	3.8	875	S62177	2	DNA topoisomerase
1099	67	3.8	876	I49152	2	HIR2 protein - yea
1100	67	3.8	898	T49492	2	protein-tyrosine k
1101	67	3.8	920	JC7313	2	hypothetical prote
1102	67	3.8	939	AE2275	2	aryl hydrocarbon r
1103	67	3.8	974	B86613	2	hypothetical prote
1104	67	3.8	974	T29545	2	zinc metalloprotei
1105	67	3.8	976	T29583	2	hypothetical prote
1106	67	3.8	980	I57936	2	hypothetical membr
1107	67	3.8	981	T18234	2	hypothetical prote
1108	67	3.8	1040	D81379	2	glutamate receptor
1109	67	3.8	1048	H64459	2	beta transducin ho
1110	67	3.8	1070	JC4593	2	transmembrane effl
1111	67	3.8	1115	IJMSNL	1	hypothetical prote
1112	67	3.8	1134	T04587	2	protein-tyrosine k
1113	67	3.8	1151	AG1717	2	neural cell adhesi
1114	67	3.8	1170	TSHUP1	2	hypothetical prote
1115	67	3.8	1264	S41603	2	probable peptidogl
1116	67	3.8	1309	BVBYD9	1	thrombospondin 1 p
1117	67	3.8	1328	T23007	2	type V adenylyl cy
1118	67	3.8	1365	T45031	2	RAD9 protein - yea
1119	67	3.8	1428	S62419	2	hypothetical prote
1120	67	3.8	1441	T13717	2	hypothetical prote
1121	67	3.8	1445	A48148	1	CRAG protein - fru
1122	67	3.8	1533	F71274	2	protein-tyrosine-p
1123	67	3.8	1589	T22668	2	hypothetical prote
1124	67	3.8	1680	T41628	2	hypothetical prote
						probable transcrip

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Index	Score	3.8	Num	Accession	Count	Description
1125	67	3.8	1723	H86557	2	polymorphic membra
1126	67	3.8	1723	E72067	2	polymorphic membra
1127	67	3.8	1732	C81601	2	polymorphic membra
1128	67	3.8	1742	S24600	2	projectin - fruit
1129	67	3.8	1790	S27772	1	vitellogenin precu
1130	67	3.8	1813	T30564	2	resistance protein
1131	67	3.8	2095	S29529	2	genome polyprotein
1132	67	3.8	2380	T29551	2	hypothetical prote
1133	67	3.8	2626	T31099	2	myosin-RhoGAP prot
1134	66.5	3.8	136	C72524	2	hypothetical prote
1135	66.5	3.8	147	JC7237	2	receptor-activity-
1136	66.5	3.8	181	AC0686	2	hypothetical prote
1137	66.5	3.8	191	AH0196	2	probable lipoprote
1138	66.5	3.8	218	D72494	2	probable thiosulfa
1139	66.5	3.8	228	AG2107	2	hypothetical prote
1140	66.5	3.8	245	T12334	2	L-ascorbate peroxi
1141	66.5	3.8	245	H71429	2	hypothetical prote
1142	66.5	3.8	250	S64849	2	hypothetical prote
1143	66.5	3.8	285	T12156	2	nodulin, isoform N
1144	66.5	3.8	301	S57531	2	transcription regu
1145	66.5	3.8	318	S61840	2	porin class PIB -
1146	66.5	3.8	328	D69452	2	conserved hypothet
1147	66.5	3.8	335	A53434	2	cell surface glyco
1148	66.5	3.8	344	IS1330	2	androgen receptor
1149	66.5	3.8	352	T09760	2	chymopapain (EC 3.
1150	66.5	3.8	358	G70026	2	conserved hypothet
1151	66.5	3.8	362	T41842	2	AcMNPV orf101 - Bo
1152	66.5	3.8	367	T06529	2	cysteine proteinas
1153	66.5	3.8	382	C86321	2	hypothetical prote
1154	66.5	3.8	384	F84675	2	hypothetical prote
1155	66.5	3.8	394	AC3364	2	glutaryl-CoA dehyd
1156	66.5	3.8	397	T34441	2	hypothetical prote
1157	66.5	3.8	404	I61596	2	advanced glycosyla
1158	66.5	3.8	413	H82270	2	hypothetical prote
1159	66.5	3.8	417	A27775	2	phosphoglycerate k
1160	66.5	3.8	422	BVBYMS	1	MSI1 protein - yea
1161	66.5	3.8	438	A97590	2	hypothetical prote
1162	66.5	3.8	438	AH2811	2	ATPase, AAA family
1163	66.5	3.8	438	A82262	2	conserved hypothet
1164	66.5	3.8	442	E65211	2	chorismate lyase u
1165	66.5	3.8	453	A89873	2	hypothetical prote
1166	66.5	3.8	461	D96835	2	probable cyclin, 4
1167	66.5	3.8	463	T26655	2	hypothetical prote
1168	66.5	3.8	475	A54879	2	pregnancy-specific
1169	66.5	3.8	491	D91217	2	ketol-acid reducto
1170	66.5	3.8	491	E86063	2	ketol-acid reducto
1171	66.5	3.8	497	JE0275	2	voltage-gated pota
1172	66.5	3.8	532	T15354	2	hypothetical prote
1173	66.5	3.8	542	A49114	2	protein-tyrosine k
1174	66.5	3.8	549	H64992	2	hypothetical prote
1175	66.5	3.8	553	T15220	2	extracellular prot
1176	66.5	3.8	557	S21596	2	Ig mu chain - shee
1177	66.5	3.8	592	S25705	2	GTP-binding protei
1178	66.5	3.8	616	G64160	2	protein C34G6.1 [i
1179	66.5	3.8	636	H87789	2	endo-1,4-beta-xyla
1180	66.5	3.8	656	S59631	1	probable formate d
1181	66.5	3.8	679	C71007	2	exo-alpha-sialidas
1182	66.5	3.8	697	B98063	2	carcinoembryonic a
1183	66.5	3.8	709	A35364	2	coat protein VP1 -
1184	66.5	3.8	718	VCPVIM	1	probable pre-mRNA-
1185	66.5	3.8	773	S46011	2	DNA topoisomerase
1186	66.5	3.8	848	C70203	2	hypothetical prote
1187	66.5	3.8	862	B36786	2	telencephalin prec
1188	66.5	3.8	917	I48950	2	ionotropic glutama
1189	66.5	3.8	921	T51136	2	meiotic recombinat
1190	66.5	3.8	923	T41350	2	protein T24P13.14
1191	66.5	3.8	969	C86394	2	probable lipoprote
1192	66.5	3.8	1005	S73711	2	glutamate receptor
1193	66.5	3.8	1009	JH0266	2	integrin alpha-v c
1194	66.5	3.8	1044	T10050	2	Xsal-3 protein - A
1195	66.5	3.8	1061	JC7116	2	phycobilisome link
1196	66.5	3.8	1080	A35088	2	hypothetical prote
1197	66.5	3.8	1097	T45622	2	hypothetical prote
1198	66.5	3.8	1117	JC4934	2	delta-crystallin/E
1199	66.5	3.8	1160	T39898	2	carbamoyl-phosphat
1200	66.5	3.8	1181	T20386	2	hypothetical prote
1201	66.5	3.8	1182	S59951	2	DNA-directed RNA p
1202	66.5	3.8	1183	H89821	2	RNA polymerase bet
1203	66.5	3.8	1184	A42904	2	adenylylcyclase ty
1204	66.5	3.8	1344	T14316	2	rig-1 protein - mo
1205	66.5	3.8	1376	F83711	2	exopolygalacturona
1206	66.5	3.8	1447	A54100	2	tumor suppressor p
1207	66.5	3.8	1462	T06819	2	DNA topoisomerase
1208	66.5	3.8	1471	F86218	2	protein F22O13.8 [
1209	66.5	3.8	1484	T42632	2	breast cancer tumo
1210	66.5	3.8	1545	T26589	2	hypothetical prote
1211	66.5	3.8	1565	T01060	2	hypothetical prote
1212	66.5	3.8	1616	T00713	2	helicase homolog F
1213	66.5	3.8	1643	T14274	2	versican precursor
1214	66.5	3.8	2089	C85426	2	ATM-like protein [
1215	66.5	3.8	2303	GNNYTM	1	genome polyprotein
1216	66.5	3.8	2470	I50726	2	cation-independent
1217	66.5	3.8	2588	AI2136	2	peptide synthetase
1218	66.5	3.8	3262	AH2137	2	hypothetical prote
1219	66.5	3.8	3305	T18358	2	apolipophorin prec
1220	66.5	3.8	3381	T42389	2	versican precursor
1221	66.5	3.8	3738	T05501	2	hypothetical prote
1222	66.5	3.8	4092	S38128	1	dynein heavy chain
1223	66.5	3.8	4436	E71086	2	hypothetical prote
1224	66.5	3.8	4447	A69679	2	polyketide synthas
1225	66.5	3.8	5147	IJFFTM	1	cadherin-related t
1226	66	3.7	118	S12627	2	Ig lambda chain pr
1227	66	3.7	132	RWMS12	1	T-cell receptor ga
1228	66	3.7	134	T52469	2	cytochrome b5 [imp
1229	66	3.7	167	S29579	2	Ig light chain - r
1230	66	3.7	182	A34647	2	pregnancy-specific
1231	66	3.7	189	A31348	1	T-cell receptor CD
1232	66	3.7	192	B75144	2	hypothetical prote
1233	66	3.7	216	S69130	2	Ig lambda chain (D
1234	66	3.7	226	T38234	2	hypothetical prote
1235	66	3.7	255	H72539	2	probable 4-nitroph
1236	66	3.7	261	G87608	2	hypothetical prote
1237	66	3.7	272	T10116	2	replication protei
1238	66	3.7	281	G71095	2	hypothetical prote
1239	66	3.7	307	A71602	2	rifin PFB0955w - m
1240	66	3.7	324	S56435	2	hypothetical 35.5K
1241	66	3.7	362	T04079	2	ferredoxin-NADP re
1242	66	3.7	376	T19186	2	hypothetical prote
1243	66	3.7	381	AE2197	2	ABC transport prot
1244	66	3.7	400	T24890	2	hypothetical prote
1245	66	3.7	406	H64793	2	ybdN protein - Esc
1246	66	3.7	406	A99709	2	hypothetical prote
1247	66	3.7	406	B85559	2	hypothetical prote
1248	66	3.7	417	S22784	2	acetyl-CoA C-acylt
1249	66	3.7	428	T14529	1	S-locus-specific g
1250	66	3.7	432	T05236	2	hypothetical prote
1251	66	3.7	448	G83818	2	hypothetical prote
1252	66	3.7	451	T30603	2	perlecan homolog 2
1253	66	3.7	457	D69059	2	glycinamide ribonu
1254	66	3.7	459	T08594	2	probable sulfate a
1255	66	3.7	466	T27120	2	hypothetical prote
1256	66	3.7	469	E70076	2	arabinan endo-1,5-
1257	66	3.7	471	S14165	2	cyclin B1 - yeast
1258	66	3.7	489	VGBTA	1	glycoprotein A - t
1259	66	3.7	495	C71679	2	UDP-n-acetylmurama
1260	66	3.7	525	S55099	2	GMP synthase (glut
1261	66	3.7	532	B34104	1	protein-tyrosine k
1262	66	3.7	532	A34104	2	protein-tyrosine k
1263	66	3.7	538	JC2457	2	vascular cell adhe
1264	66	3.7	545	D81973	2	probable integral
1265	66	3.7	550	I37579	2	DiGeorge syndrome
1266	66	3.7	553	T48486	2	hypothetical prote
1267	66	3.7	580	H72270	2	ABC transporter, A
1268	66	3.7	589	B90605	2	hypothetical prote
1269	66	3.7	592	E70455	2	sulfur oxidation p
1270	66	3.7	603	S03020	2	dopamine beta-mono

Index	Score	%	Accession	N	Length	Description
1271	3.7	66	D84986	2	624	heat shock protein
1272	3.7	66	I52257	2	631	episialin - mouse
1273	3.7	66	B96784	2	640	hypothetical prote
1274	3.7	66	T23271	2	662	hypothetical prote
1275	3.7	66	G81970	2	687	probable glycine-t
1276	3.7	66	S44237	2	719	trypomastigote sur
1277	3.7	66	A40096	2	738	platelet-endotheli
1278	3.7	66	S66959	2	747	hypothetical prote
1279	3.7	66	T04010	2	750	hypothetical prote
1280	3.7	66	T01449	2	751	cytoskeletal prote
1281	3.7	66	JC4898	2	754	Down-syndrome-crit
1282	3.7	66	D81924	2	808	hemeoglobin-haptog
1283	3.7	66	A81965	2	810	hypothetical prote
1284	3.7	66	T35970	2	815	probable efflux pr
1285	3.7	66	T49782	2	833	related to alkalin
1286	3.7	66	T16753	2	839	hypothetical prote
1287	3.7	66	T47495	2	851	hypothetical prote
1288	3.7	66	AE0525	2	863	outer membrane ush
1289	3.7	66	H85335	2	864	hypothetical prote
1290	3.7	66	T04518	2	864	hypothetical prote
1291	3.7	66	AE0519	2	901	preprotein translo
1292	3.7	66	A60560	2	902	formyltetrahydrofo
1293	3.7	66	IJCHCN	1	912	N-cadherin precurs
1294	3.7	66	B84640	2	920	probable ligand-ga
1295	3.7	66	G90053	2	961	hypothetical prote
1296	3.7	66	A72012	2	974	metalloproteinase,
1297	3.7	66	I45877	2	977	protein-tyrosine k
1298	3.7	66	JH0589	2	979	glutamate receptor
1299	3.7	66	JH0592	2	979	glutamate receptor
1300	3.7	66	AD2195	2	1006	hypothetical prote
1301	3.7	66	T15191	2	1043	hypothetical prote
1302	3.7	66	S72194	2	1053	hydroxymethylgluta
1303	3.7	66	H95321	2	1065	NolG efflux transp
1304	3.7	66	A35007	2	1100	ATP citrate (pro-S
1305	3.7	66	S21173	2	1105	ATP citrate (pro-S
1306	3.7	66	T30202	2	1112	probable chitin sy
1307	3.7	66	S44641	2	1118	hypothetical prote
1308	3.7	66	T22811	2	1139	Lin-25 protein - C
1309	3.7	66	T52459	2	1207	sensory transducti
1310	3.7	66	S29717	2	1223	adenylate cyclase
1311	3.7	66	T43027	2	1232	neural cell adhesi
1312	3.7	66	T39453	2	1242	probable mrna stab
1313	3.7	66	C89874	2	1248	autolysin [importe
1314	3.7	66	T30211	2	1335	autolysin E - Stap
1315	3.7	66	T26301	2	1353	hypothetical prote
1316	3.7	66	S44241	2	1363	surface protein -
1317	3.7	66	A41228	2	1367	protein-tyrosine k
1318	3.7	66	D86338	2	1549	protein F5M15.18 [
1319	3.7	66	T18800	2	1601	hypothetical prote
1320	3.7	66	G84649	2	1750	hypothetical prote
1321	3.7	66	T08878	2	1792	supervillin P205 -
1322	3.7	66	T14106	2	1822	probable GTPase-ac
1323	3.7	66	T41455	2	1828	cut1 protein - fis
1324	3.7	66	T30902	2	1993	sodium channel SCA
1325	3.7	66	AC0233	2	2035	yersiniabactin bio
1326	3.7	66	T17439	2	2041	peptide synthetase
1327	3.7	66	H89960	2	2186	hypothetical prote
1328	3.7	66	TVHURS	1	2347	kinase-related pro
1329	3.7	66	T30201	2	2352	Notch homolog prot
1330	3.7	66	A46105	2	3415	polyprotein(NS1, N
1331	3.7	66	T16580	2	13055	hypothetical prote
1332	3.7	65.5	OGBO6A	1	98	cytochrome-c oxida
1333	3.7	65.5	JN0032	2	105	early protein gp12
1334	3.7	65.5	S17719	2	130	H+-transporting tw
1335	3.7	65.5	RWRBAV	1	134	T-cell receptor al
1336	3.7	65.5	S04934	2	166	T-cell receptor de
1337	3.7	65.5	H81285	2	178	probable flagellar
1338	3.7	65.5	QQBEC6	1	186	HQLF1 precursor -
1339	3.7	65.5	T29925	2	194	hypothetical prote
1340	3.7	65.5	JC5626	2	198	DNA helicase-prima
1341	3.7	65.5	JC5760	2	198	STAT induced STAT
1342	3.7	65.5	E96912	2	200	cytokine-inducible
1343	3.7	65.5	A36462	2	223	adenylylsulfate ki

Description	Accession	N	Length	Score	%	Index
heat shock protein	G87286	2	237	3.7	65.5	1344
coat protein - tob	VCCVTY	1	254	3.7	65.5	1345
conserved hypothet	A69077	2	276	3.7	65.5	1346
hypothetical prote	H90409	2	283	3.7	65.5	1347
heat shock protein	B82534	2	289	3.7	65.5	1348
UDP-N-acetylenolpy	A75497	2	290	3.7	65.5	1349
concanavalin A pre	A34139	2	290	3.7	65.5	1350
rifin PFB0065w - m	G71623	2	309	3.7	65.5	1351
sporulation protei	A29812	2	311	3.7	65.5	1352
conserved hypothet	F69820	2	312	3.7	65.5	1353
probable chemotaxi	G71864	2	323	3.7	65.5	1354
probable oligopept	F71130	2	331	3.7	65.5	1355
iron(III) dicitrat	AD2134	2	336	3.7	65.5	1356
Fit-1S protein pre	S42632	2	344	3.7	65.5	1357
probable binding p	F83620	2	379	3.7	65.5	1358
formate dehydrogen	E64300	2	383	3.7	65.5	1359
hypothetical 39.2K	S47711	2	383	3.7	65.5	1360
hypothetical prote	C86020	2	386	3.7	65.5	1361
hypothetical prote	C91174	2	393	3.7	65.5	1362
hypothetical prote	T25755	2	398	3.7	65.5	1363
glutaryl-CoA dehyd	D83589	1	399	3.7	65.5	1364
Ig gamma-3 chain C	G3MSM	2	405	3.7	65.5	1365
formate dehydrogen	B24698	2	407	3.7	65.5	1366
two-component syst	D82542	2	409	3.7	65.5	1367
hypothetical prote	A71613	1	410	3.7	65.5	1368
alanine transamina	T14611	1	410	3.7	65.5	1369
aminopeptidase amp	C69585	1	411	3.7	65.5	1370
aminopeptidase BH2	B83930	1	411	3.7	65.5	1371
P1 polyprotein - m	QQCVPZ	2	414	3.7	65.5	1372
hypothetical prote	F64224	2	429	3.7	65.5	1373
hypothetical prote	E90572	2	430	3.7	65.5	1374
hypothetical prote	S27793	1	440	3.7	65.5	1375
hypothetical prote	G89962	2	447	3.7	65.5	1376
TyA protein - yeas	S45737	2	452	3.7	65.5	1377
TyA protein - yeas	S49765	2	486	3.7	65.5	1378
hypothetical prote	T28207	2	487	3.7	65.5	1379
probable respirato	T39761	2	489	3.7	65.5	1380
conserved hypothet	D70439	1	506	3.7	65.5	1381
hypothetical cell	AI1505	2	527	3.7	65.5	1382
EcoA system protei	A47200	2	545	3.7	65.5	1383
hypothetical prote	D71461	2	555	3.7	65.5	1384
hypothetical prote	S37899	2	561	3.7	65.5	1385
protein F47D12.9 [	B88479	2	564	3.7	65.5	1386
inositol-3-phospha	A30902	1	566	3.7	65.5	1387
high mobility grou	S35637	2	575	3.7	65.5	1388
hypothetical prote	A89956	2	582	3.7	65.5	1389
probable ubiquitin	F84903	2	585	3.7	65.5	1390
methyl-accepting c	S46692	2	608	3.7	65.5	1391
hypothetical prote	H97326	2	615	3.7	65.5	1392
hypothetical prote	B83218	2	621	3.7	65.5	1393
dihydrofolate redu	RDZQK1	1	623	3.7	65.5	1394
hypothetical prote	T29223	2	638	3.7	65.5	1395
hypothetical prote	T20863	2	647	3.7	65.5	1396
putaive autotransp	AD2295	2	649	3.7	65.5	1397
dnaK-type molecula	AH0340	2	656	3.7	65.5	1398
hypothetical prote	HHXL70	1	672	3.7	65.5	1399
probable serine/th	T05630	2	683	3.7	65.5	1400
hypothetical prote	B86289	2	694	3.7	65.5	1401
TonB-dependent rec	S75001	2	714	3.7	65.5	1402
exo-alpha-sialidas	D82674	2	714	3.7	65.5	1403
probable portal pr	I40866	2	743	3.7	65.5	1404
probable portal pr	E90781	2	755	3.7	65.5	1405
probable bi-functi	B85642	2	761	3.7	65.5	1406
probable ABC trans	T34632	2	782	3.7	65.5	1407
hypothetical prote	G84791	2	787	3.7	65.5	1408
hypothetical prote	S66719	2	789	3.7	65.5	1409
hypothetical prote	A82940	2	852	3.7	65.5	1410
DNA helicase-prima	C84898	2	874	3.7	65.5	1411
hypothetical prote	S55639	2	899	3.7	65.5	1412
translation elonga	T21362	2		3.7	65.5	1413
hypothetical prote	A40411	2		3.7	65.5	1414
hypothetical prote	T29548	2		3.7	65.5	1415
core protein VP3 -	P3XREH	1		3.7	65.5	1416

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1417 2  921 3.7 65.5 S49965 probable membrane
1418 2  946 3.7 65.5 A47299 ror-related recept
1419 2  948 3.7 65.5 C75265 hexagonally packed
1420 2  953 3.7 65.5 E84732 probable ligand-ga
1421 2  956 3.7 65.5 JS0685 glutamate receptor
1422 2 1051 3.7 65.5 G84416 ribonucleoside red
1423 2 1052 3.7 65.5 B49120 protein-tyrosine k
1424 2 1054 3.7 65.5 D70425 conserved hypothet
1425 2 1066 3.7 65.5 AB1228 transporter, (to B
1426 2 1066 3.7 65.5 AD1581 transporter, (to B
1427 2 1068 3.7 65.5 JQ1329 sucrose-phosphate
1428 1 1084 3.7 65.5 B64088 hemoglobin-binding
1429 1 1091 3.7 65.5 A58532 glial cell membran
1430 1 1100 3.7 65.5 DDBYD1 RAD1 protein - yea
1431 2 1125 3.7 65.5 H87644 TonB-dependent rec
1432 2 1132 3.7 65.5 AD1809 phycobilisome core
1433 2 1174 3.7 65.5 A40853 potassium channel
1434 2 1259 3.7 65.5 S36126 neural cell adhesi
1435 2 1270 3.7 65.5 T51227 related to verruco
1436 2 1464 3.7 65.5 JC5144 murinoglobulin pre
1437 2 1476 3.7 65.5 JC5143 alpha-macroglobuli
1438 2 1487 3.7 65.5 AG2560 hypothetical prote
1439 2 1657 3.7 65.5 T15838 hypothetical prote
1440 2 1744 3.7 65.5 JH0720 tanabin - African
1441 2 1755 3.7 65.5 S45736 TyB protein - yeas
1442 2 1871 3.7 65.5 S27938 hypothetical prote
1443 2 2062 3.7 65.5 G96602 probable receptor
1444 1 2311 3.7 65.5 TVCHSR kinase-related pro
1445 2 2386 3.7 65.5 T39911 rad3 checkpoint pr
1446 2 3135 3.7 65.5 A48584 transmission block
1447 2 3147 3.7 65.5 T21328 hypothetical prote
1448 2 4302 3.7 65.5 A38971 polycystic kidney
1449 1   61 3.7 65   F26420 T-cell receptor ga
1450 1  115 3.7 65   KVMSK2 Ig kappa chain pre
1451 1  128 3.7 65   KVMST1 Ig kappa chain pre
1452 1  140 3.7 65   I46638 rearranged T-cell
1453 2  158 3.7 65   D83809 transcription elon
1454 2  216 3.7 65   JE0245 Ig lambda chain NI
1455 1  219 3.7 65   T02114 hypothetical prote
1456 1  231 3.7 65   A29459 orotate phosphorib
1457 2  235 3.7 65   S25758 Ig lambda chain -
1458 2  244 3.7 65   I62393 outer membrane pro
1459 2  244 3.7 65   I62389 outer membrane pro
1460 1  255 3.7 65   S48146 mucin 1 precursor,
1461 2  273 3.7 65   T42928 immediate-early pr
1462 2  308 3.7 65   C84072 UDP-glucose 4-epim
1463 2  313 3.7 65   B69588 L-arabinose transp
1464 2  322 3.7 65   PS0019 Ig gamma-2a chain
1465 2  331 3.7 65   G91133 probable collagena
1466 2  331 3.7 65   B85979 probable collagena
1467 2  331 3.7 65   B65106 probable proteinas
1468 2  345 3.7 65   A46052 vascular cell adhe
1469 1  349 3.7 65   A28658 nitrilase (EC 3.5.
1470 2  350 3.7 65   D84923 probable exonuclea
1471 2  354 3.7 65   A81728 conserved hypothet
1472 2  355 3.7 65   S21057 recF protein - Sal
1473 2  358 3.7 65   G70601 hypothetical prote
1474 2  363 3.7 65   B65057 hypothetical prote
1475 1  373 3.7 65   VGBETC glycoprotein A - t
1476 1  388 3.7 65   EHMS   Ig epsilon chain C
1477 2  392 3.7 65   S04205 protein-tyrosine k
1478 2  394 3.7 65   B70411 fimbrial assembly
1479 2  397 3.7 65   T31803 hypothetical prote
1480 2  404 3.7 65   F86517 hypothetical prote
1481 2  404 3.7 65   G72106 hypothetical prote
1482 2  412 3.7 65   E65146 hypothetical 47.4
1483 2  414 3.7 65   S43340 glyceraldehyde-3-p
1484 1  414 3.7 65   AE1500 N-carbamyl-L-amino
1485 2  416 3.7 65   A42879 advanced glycosyla
1486 2  425 3.7 65   D70436 DNA mismatch repai
1487 1  432 3.7 65   RWCZT4 T-cell surface gly
1488 1  443 3.7 65   E64667 multidrug-efflux t
1489 2  443 3.7 65   T17970 hypothetical prote
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1490 65 3.7 444 1 DYBOD2 dopamine receptor
1491 65 3.7 444 2 PC4436 monoclonal antibod
1492 65 3.7 449 2 A69643 serine proteinase
1493 65 3.7 451 2 T33763 hypothetical prote
1494 65 3.7 452 2 G95306 putrescine/ornithi
1495 65 3.7 468 2 T49682 hypothetical prote
1496 65 3.7 469 2 S50584 probable phosphogl
1497 65 3.7 487 2 AI2692 conserved hypothet
1498 65 3.7 487 2 E97474 BH3939 hypothetica
1499 65 3.7 493 2 T01206 cysteine proteinas
1500 65 3.7 494 2 A35551 cytochrome P450 2G
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ALIGNMENTS

RESULT 1
A46500
Ly-9.2 antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46500
R;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.
J. Immunol. 149, 1636-1641, 1992
A;Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A;Reference number: A46500; MUID:92373005; PMID:1506686
A;Accession: A46500
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-629 <SAN>
A;Cross-references: UNIPARC:UPI0000047632; GB:M84412; NID:g198931; PIDN:AAA39468.1; PID
A;Experimental source: C57BL/6
A;Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C;Keywords: transmembrane protein

Query Match   19.4%; Score 343; DB 2; Length 629;
Best Local Similarity 29.3%; Pred. No. 2.7e-20;
Matches 105; Conservative 58; Mismatches 143; Indels 52; Gaps 14;

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Qy  14 LWQL-TGSA----ASGPVKELVGSVGGAVTFPLKSK-VKQVDSIVWTFNTTPLVTIQPEG  67
          ::| :::      |:|          :| |||| :|   :|| :|||||:::   :|
Db 217 IWQFCTGASRRKTAAG--KTVVGILGEPVTLPLEFRATRATKNVVWLNTS--VISQRR   272

Qy  68 GTIIVTQNR-----NRERVDFPDGGYSLKLSKLKKNDSGIYVGIYSSSLQQPSTQEYVL 122
          :::    :|     |:: : :|| |||:|| ||: :|| || :|:  :|  :| || 
Db 273 GAATADSRRKPKGSEBRRVRTSDQDQSLKISQLKMEDAGPYHAYVCSSASRDPSVRHFTL 332

Qy 123 HVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPI 182
        ||: | |||| || |:|:||| ||::|:|::   ||:|:|:|   | |: |:|:|:|  |
Db 333 LVYKRLEKPSVTKSPVHMMNGICEVVLTCSVDGGGNNVTYTWMPLQNKAVMSQGKSHLNV 392

Qy 183 SWRWGESDMTFICVARNPVSRNFSSPILARKLCEGADDPDSSMVLLCLLLVPLLLSLFV 242
        ||  ||     | |:|||| :|:|| ::    :||               |||||:|:
Db 393 SWESGEHLPNFTCTAHNPVS-NSSSQPSSGTICSG----PERNKRFWLLLLLLLMLI   447

Qy 243 LGLFLWFLKRERRQEBYIEEK-KRVDICRETPNICPHSG-----------------ENTE 283
        :| | |||:|::|:| ::::   :|:|                               |
Db 448 GGYFI--LRKKKQCSSLATRYRQAEVPAEIPE--PPTGHGQFSVLSQRYEKLDMSAKTTR 503

Qy 284 Y------DTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db 504 HQPTPTSDTSSESSATTEEDDEKTRMHSTANSRNQL---YDLVTHQDIAHALAYEGQV 558
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RESULT 2
S58892
signaling lymphocytic activation molecule - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58892
R;Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.; de Vries, J.E.; Aversa, G.
Nature 376, 260-263, 1995
A;Title: A novel receptor involved in T-cell activation.

A;Reference number: S58892; MUID:95342241; PMID:7617038
A;Accession: S58892
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-335 <COC>
A;Cross-references: UNIPROT:Q13291; UNIPARC:UPI000047630; EMBL:U33017; NID:g984968; PID

Query Match   10.3%;   Score 182.5;   DB 2;   Length 335;
Best Local Similarity   22.5%;   Pred. No. 2.1e-07;
Matches   82;   Conservative   72;   Mismatches   129;   Indels   81;   Gaps   19;

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Qy     8 LTLIYILW-QLTGSAASGP-------VKELVGSVGGAVTFPL------KSKVKQVDSIVWT  54
           ::  : | |  :::||   ::|  :  |  |  : ::|
Db     7 LSLTFVLFLSLAFGASYGTGGRMMNCPKILRQLGSKVLLFLTYERINKSMNKSIHIVVTM  66

Qy    55 FNT------TPLVTIQP-EGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGI  107
            :|      |  :||::|    ||:||:|| |||  | |||:| |:| ||||::|||
Db    67 AKSLENSVENKIVSLDPSEAG---PPRYLGDRYKFYLENLTLGIRESRKEDEGWYLMTL  122

Qy   108 YSS-SLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTW--  164
            |:| :|:|| : | |:|  ||||::|  |  :|||| |||   ||| | | | ::|
Db   123 EKNVSVQRFCLQ--LRLYEQVSTPEIKVLNKTQENGTCTLILGCTVEKGDH-VAYSWSE  178

Qy   165 KALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP  222
            | |  | ||||:|   :  |:|:|||||||||||||||||  |||||||||||||||
Db   179 KAGTHPLNPANSSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP------WPGCRTDP  232

Qy   223 DSSM------------VLLCLLVPLLLSLFVLGLFLWFLKREREQEYIE--EKKRVDIC  268
            |::|            | |:  ::|  :  |  :  | | |      ||  ||||:|||
Db   233 SETKPWAVYAGLLGGVIMILIMVVIIQ-----------LRRRGKTNHYQTTVEKKSLTIY  281

Qy   269 RETPNICPHSGENTEYDTIPHTNRTTLKEDPANTVY--STVEIPKKMENPHSL------LT  321
            | :|:| :|:: ::||:  | | | ::|  :  ::| |:|    |  :      :|
Db   282 AQVQKPGP--LQKKLDSFP-------AQDPCTTIYVAATEPVPESVQETNSITVYASVT  331

Qy   322 MPDT  325
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Db   332 LPES  335
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RESULT 3
B28967
T-cell surface glycoprotein CD2 precursor - mouse
N;Alternate names: CD2 antigen; T-lymphocyte antigen CD2; T11 protein
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
C;Accession: B28967; S01347; S02293
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A;Reference number: A28967; MUID:88144486; PMID:2894031
A;Accession: B28967
A;Molecule type: mRNA
A;Residues: 1-344 <DIA>
A;Cross-references: UNIPROT:Q9R201; UNIPARC:UPI00000E898A; GB:M19807; NID:g192479; PIDN:
A;Note: the authors translated the codon TAT for residue 99 as Thr
R;Clayton, L.K.; Sayre, P.H.; Novotny, J.; Reinherz, E.L.
Eur. J. Immunol. 17, 1367-1370, 1987
A;Title: Murine and human T11 (CD2) cDNA sequences suggest a common signal transduction
A;Reference number: S01347; S02293
A;Accession: S01347
A;Molecule type: mRNA
A;Residues: 1-127,'M',129-174,'N',176-190,'N','M',193-344 <CLA>
A;Cross-references: UNIPARC:UPI000016D064; EMBL:X06143; NID:g54223; PIDN:CAA29500.1; PID
R;Sewell, W.A.; Brown, M.H.; Owen, M.J.; Fink, P.J.; Kozak, C.A.; Crumpton, M.J.
Eur. J. Immunol. 17, 1015-1020, 1987
A;Title: The murine homologue of the T lymphocyte CD2 antigen: molecular cloning, chromc
A;Reference number: S02293; MUID:87276135; PMID:2440689
A;Accession: S02293
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-127,'M',129-174,'N',176-191,'M',193-344 <SEW>
A;Cross-references: UNIPARC:UPI00000019C; EMBL:Y00023; NID:g50346; PIDN:CAA68258.1; PID

C;Genetics:
A;Map position: 3
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; surface antigen; T-cell; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-344/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;23-203/Domain: extracellular #status predicted <EXT>
F;204-228/Domain: transmembrane #status predicted <TMM>
F;229-344/Domain: intracellular #status predicted <INT>

Query Match   8.1%;   Score 144;   DB 2;   Length 344;
Best Local Similarity   21.4%;   Pred. No. 0.00033;
Matches   72;   Conservative   56;   Mismatches   132;   Indels   76;   Gaps   16;

```
Qy    12 YILWQLTGSAASGPVKELV-GSVGGAVT-FPLKSKVKQVDSIVWTFNTTPLVTIQPEGG  68
           ::| | |    |  :||  |  | |:  |     | : |  ||:|
Db    10 FLLFSLSGKGADCRDNETIWGVLGHGITLNIPNFQMTDDIDEVRWV-----------RRG  58

Qy    69 TIIVTQNRNR------ERVDFPDGGYSLKLSK-LKKNDSGIYYVGIYSSSLQQPSTQEYV  121
           ::: |        | :|| || | ||:|::|  |  ::||:||  ||
Db    59 TLVAEFKRKKPPFLISETYEVLANG-SLKIKKKPMMRNDSGTYNVMVYGTNGMTRLEKDLD  117

Qy   122 LHVYEHLSKPKVTMGLQSNKNGTCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL  180
            |     :  ::|  |:    | | |  |||  |
Db   118 VRILERVSKPVI-------------HWECPNTTLTCAVLQGTDFELKLYQ-GETLLNS----L  162

Qy   181 P---ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCL------  231
```

RESULT 4
I49585
CD2 antigen protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-1996
C;Accession: I49585
R;Yagita, H.; Okumura, K.; Nakauchi, H.
J. Immunol. 140, 1321-1326, 1988
A;Title: Molecular cloning of the murine homologue of CD2: Homology of the molecule to i
A;Reference number: I49585; MUID:88140313; PMID:3257775
A;Accession: I49585
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA <RES>
A;Residues: 1-344
A;Cross-references: UNIPROT:P08920; UNIPARC:UPI000016CC8E; GB:M18934; NID:g192486; PIDN:
C;Superfamily: T-cell surface glycoprotein CD2

Query Match   7.8%;   Score 138;   DB 2;   Length 344;
Best Local Similarity   21.1%;   Pred. No. 0.001;
Matches   71;   Conservative   56;   Mismatches   133;   Indels   76;   Gaps   16;

```
Qy    12 YILWQLTGSAASGPVKELV-GSVGGAVT-FPLKSKVKQVDSIVWTFNTTPLVTIQPEGG  68
           ::| | |    |  :||  |  | |:  |     | : |  ||:|
Db    10 FLLFSLSGKGADCRDNETIWGVLGHGITLNIPNFQMTDDIDEVRWV-----------RRG  58

Qy    69 TIIVTQNRNR------ERVDFPDGGYSLKLSK-LKKNDSGIYYVGIYSSSLQQPSTQEYV  121
           ::: |        | :|| || | ||:|::|  |  ::||:||  ||
Db    59 TLVAEFKRKKPPFLISETYEVLANG-SLKIKKKPMMRNDSGTYNVMVYGTNGMTRLEKDLD  117

Qy   122 LHVYEHLSKPKVTMGLQSNKNGTCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL  180
            |     :  ::|  |:    | | |  |||  |
Db   118 VRILERVSKPVI-------------HWECPNTTLICAVLQGTDFELKLYQ-GETLLNS----L  162

Qy   181 P---ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCL------  231
```

```
Db   163 PQKMSYQWTNLSAPFKCEAINPVSKESKTEVV------NCPEKGLSFYVTVGVGAG 213
                  :|:||       |     ||:   :|         ||||

Qy   232 -LLVPLLLSLFVLGLFLWFLKRERQEBYIEEKKRVDICRETPNICPHSGENTEYDTIPHT 290
              :|:||||:|:||:       |:| | |             ||:

Db   214 GLLLVLIVALFI---FCICKRRKRNRRKDEELEIKASRTS-------TVERGPKPHS 261
             ||      ||:    :|

Qy   291 NRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTP 326

Db   262 T------PAAAAQNSVALQAPPPGGHHLQTPGHRP 290
```

RESULT 5
RWHUC2
T-cell surface glycoprotein CD2 precursor - human
N;Alternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A28967; A26486; B26486; A28416; A28023; S02292; A30430; S00829; A29874
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A;Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A;Reference number: A28967; MUID:88144486; PMID:2894031
A;Accession: A28967
A;Molecule type: DNA
A;Residues: 1-351 <DIA>
A;Cross-references: UNIPROT:P06729; UNIPARC:UPI000062209; GB:M19806; GB:J03622; GB:J036
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A;Reference number: A26486; MUID:87041523; PMID:3490670
A;Accession: A26486
A;Molecule type: mRNA
A;Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SE1>
A;Cross-references: UNIPARC:UPI000004D168
A;Accession: B26486
A;Molecule type: protein
A;Residues: 25-46,'X',50 <SE2>
A;Cross-references: UNIPARC:UPI000004D168
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A;Reference number: A28416
A;Contents: revision
A;Accession: A28416
A;Molecule type: mRNA
A;Residues: 333-351 <SE3>
A;Cross-references: UNIPARC:UPI000173764
R;Seed, B.; Aruffo, A.
Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987
A;Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap
A;Reference number: A28023; MUID:87204137; PMID:2437578
A;Accession: A28023
A;Molecule type: mRNA
A;Residues: 1-265,'Q',267-351 <SEE>
A;Cross-references: UNIPARC:UPI000127347; GB:M16445; NID:g178668; PIDN:AAA51738.1; PID:
R;Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987
A;Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure
A;Reference number: S02292; MUID:87204243; PMID:2883656
A;Accession: S02292
A;Molecule type: mRNA
A;Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SA1>
A;Cross-references: UNIPARC:UPI000004D168
A;Accession: A30430
A;Molecule type: protein
A;Residues: 25-43,152-163 <SA2>
A;Cross-references: UNIPARC:UPI000173765
R;Lang, G.; Wotton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.
EMBO J. 7, 1675-1682, 1988
A;Title: The structure of the human CD2 gene and its expression in transgenic mice.
A;Reference number: S00829; MUID:89050055; PMID:2901953
A;Accession: S00829
A;Molecule type: DNA

A;Residues: 1-351 <LAN>
A;Cross-references: UNIPARC:UPI000062209; EMBL:X07871
C;Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appea
or is closely associated with, the erythrocyte receptor.
C;Genetics:
A;Gene: GDB:CD2
A;Cross-references: GDB:118735; OMIM:186990
A;Map position: 1p13.1-1p13.1
A;introns: 21/1; 128/1; 205/1; 246/1
A;introns: 21/1; 128/1; 246/1
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;25-206/Domain: extracellular #status predicted <EXT>
F;210-234/Domain: transmembrane #status predicted <TMM>
F;237-351/Domain: intracellular #status predicted <INT>
F;89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   7.7%;   Score 136.5;   DB 1;   Length 351;
Best Local Similarity   23.9%;   Pred. No. 0.0014;
Matches   71;   Conservative   44;   Mismatches   111;   Indels   71;   Gaps   15;

```
Qy    28 ELVGSVGGAVTFPLKS--KVKQVDSIVW--TFNTTPLVTIQPEGGTIIVTQNRNRERVDF 83
            :  |   |: :|       |   |::

Db    32 ETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETF---KEKDTYKL-F 87

Qy    84 PDDGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEVVLHVELVLHVHLSKPKVTMGLQSNKNG 143
            :  |  :|| | | |:|| :| : ::|  ||::| :::||

Db    88 KNG--TLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQERVSKPKISW------- 137

Qy   144 TCV-TNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWR-----WGES-DMTFICV 196
            || :|||||: :|  | | |         | |

Db   138 TCINTTLTCEVMNGTDPEL----------NLYQDGKHLKLSQRVITHKWTTSLSAKFKCT 187

Qy   197 ARNPVSRNFS-SPI---------LARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGL 245
            | | ::       :|           |

Db   188 AGNKVSKESSVEPVSCPEKGLDIYLIIGICGGGS---------------LLMVFVALL 230

Qy   246 FLWFLKRERQEBYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRRTILKEDPANT 302
            : :|||:            |

Db   231 VPYITKRKKQ----RSRRNDELETR--AHRVATERGRKPHQIPASTPQNPATS 279
```

RESULT 6
S01299
OX-45 membrane glycoprotein precursor - rat
N;Alternate names: MRC OX-45 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
A;Accession: S01299
R;Killeen, N.; Moessner, R.; Arvieux, J.; Willis, A.; Williams, A.F.
EMBO J. 7, 3087-3091, 1988
A;Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the
A;Reference number: S01299; MUID:89030603; PMID:3181129
A;Accession: S01299
A;Molecule type: mRNA
A;Residues: 1-240 <KIL>
A;Cross-references: UNIPROT:P10252; UNIPARC:UPI000127370; EMBL:X13016; NID:g56804; PID:
C;Superfamily: B-cell surface glycoprotein blast-1
C;Keywords: glycoprotein; membrane protein; surface antigen
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-240/Product: OX-45 membrane glycoprotein #status predicted <MAT>
F;38,97,140,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   7.6%;   Score 134;   DB 2;   Length 240;
Best Local Similarity   24.6%;   Pred. No. 0.0014;
Matches   48;   Conservative   33;   Mismatches   104;   Indels   10;   Gaps   4;

```
Qy    13 ILWQLTGSAASGPVKELVGSV---GGAVTFP-LKSKVKQVDSIVWTFNTTPLVTIQPEG 67
            |:  | :: |     :|| ||      ||| | :: :||

Db    11 ILESLLLSLVTGFQDQSVPNVNAITGSNVTLTILKHPLASYQRLTWLHTTNQKILEYPPN 70

Qy    68 GTIIVTQNRNRERVDFPDPGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEVLHVVEH 127
```

```
Db    166  ---MSYQWTNLRAPFKCKAVNRVSQESEMEVV--------NCPEKGLPLYLIVGVSAG 212
                :|:||                                            :: :|||::
Qy    237  -LLSLFVLGLFLWFL------KRERQEEYIEEK-KRVDICRETPNICPHS 278
             ||:||: ||||:|              ||:|:|        |||
Db    213  GLLLVFFGALFIFCICKRKKRNRRRKGEELEIKASRMSTVERGPK--PHS 260
```

RESULT 8
JL0143
antigen BCM1 precursor - mouse
N;Alternate names: CD48 antigen homolog sgp-60; OX45 antigen, Blast-1 antigen
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JL0143; S21319; A47469; B47469
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
J. Exp. Med. 171, 2115-2130, 1990
A;Title: Structure, expression, and genetic linkage of the mouse BCM1 (OX45 or Blast-1
region on mouse chromosome 3.
A;Reference number: JL0143; MUID:90278362; PMID:1693656
A;Accession: JL0143
A;Molecule type: mRNA
A;Residues: 1-240 <WON>
A;Cross-references: UNIPROT:P18181; UNIPARC:UPI000003EBF; EMBL:X17501; NID:g50134; PIDN
R;Wong, Y.W.; Williams, A.F.; Kingsmore, S.F.; Seldin, M.F.
submitted to the EMBL Data Library, June 1990
A;Description: Structure, expression and genetic linkage of the mouse BCM1 (OX45 or Blas
3 region on mouse chromosome 3.
A;Reference number: S21319
A;Accession: S21319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-240 <WON2>
A;Cross-references: UNIPARC:UPI000003EBF; EMBL:X53526; NID:g50138; PIDN:CAA37604.1; PID
R;Cabrero, J.G.; Freeman, G.J.; Lane, W.S.; Reiser, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 3418-3422, 1993
A;Title: Identification, by protein sequencing and gene transfection, of sgp-60 as the m
A;Reference number: A47469; MUID:93234508; PMID:8475091
A;Accession: A47469
A;Molecule type: protein
A;Residues: 74-80 <CAB>
A;Cross-references: UNIPARC:UPI000176785
A;Experimental source: EL-4 lymphoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:129658)
A;Accession: B47469
A;Molecule type: protein
A;Residues: 84-98 <CA2>
A;Cross-references: UNIPARC:UPI000176786
A;Experimental source: EL-4 lymphoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:129660)
C;Comment:This antigen is widely expressed on leukocytes and is likely to be anchored t
C;Superfamily: B-cell surface glycoprotein blast-1
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-217/Product: antigen BCM1 #status predicted <MAT>
F;218-240/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F;32,38,70,136,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;217/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match   7.1%; Score 126.5; DB 2; Length 240;
Best Local Similarity 21.4%; Pred. No. 0.0058;;
Matches   52; Conservative 45; Mismatches 125; Indels 21; Gaps   8;

```
Qy      7  CLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPL-KSKVKQVDSIWTFNTTPLVTIQP 65
              :   :||: ::|| ::   |    |||| ||||   :||| :||::  |:||
Db      9  CLVLELLLLPLGTGFQGHSIPDINATTGSNVTLKIIHKDPLGPYKRITWLHTKNQKILEYN 68
               ::|: |::  |||   :  |||        | | |   | |   |   |
Qy     66  EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKNDSGIYVVGIYSSSLQQPSTQ-EYVLHV 124
              ||  ::|:|:|   |  ||||| |  | | |   || || :::  :|   |
Db     69  YNSTKTIFESEFKGRVYLEENGALHISNVRKEDKGTYYMRV----LRETENELKITLEV 124
                     :|| :  |||  :|      | ||   | |      |   ::|  :|
Qy    125  YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISW 184
```

```
Db     71  GKKTVFESVFKDRVDLDKTNGALRIYNVSKEDRGDYYMRMLHETEDQ---WKITMEVYDL 127
              ||:|    || :|:|  :|||   ::|| | | |  ||            |::| |:|
Qy    128  LSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWG 187
              ||:||     |:| ||   ||  | |||| |||  || :|  | |    :||  :| |
Db    128  VSKPAIKIEKTKNLTDSCHLRLSCKVE--DQGVDTWYEDSGPFPQRNPGYVLEITITPH 185
```

```
Qy    188  ESDMTFICIVARNPVS 202
              ||:|| |   |||:
Db    186  NKSTFYTCQVSNPVS 200
```

RESULT 7
RWRTC2
T-cell surface glycoprotein CD2 precursor - rat
N;Alternate names: CD2 antigen; OX-34 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 25-Oct-1996
C;Accession: A33071; B27560; A27560; A32346
R;Barclay, A.N.; Williams, A.F.
submitted to the EMBL Data Library, May 1987
A;Reference number: A33071
A;Accession: A33071
A;Molecule type: mRNA
A;Residues: 1-344 <BAR>
A;Cross-references: UNIPARC:UPI000017766
R;Williams, A.F.; Barclay, A.N.; Clark, S.J.; Paterson, D.J.; Willis, A.C.
J. Exp. Med. 165, 368-380, 1987
A;Title: Similarities in sequences and cellular expression between rat CD2 and CD4 antig
A;Reference number: A27560; A27560; A32346
A;Accession: A27560
A;Molecule type: protein
A;Residues: 44-404 <WI2>
A;Cross-references: UNIPARC:UPI000017767; UNIPARC:UPI000017767; UNIPARC:UPI000017769;
A;Note: 112-Asn was also found
R;He, Q.; Beyers, A.D.; Barclay, A.N.; Williams, A.F.
Cell 54, 979-984, 1988
A;Title: A role in transmembrane signaling for the cytoplasmic domain of the CD2 T lymph
A;Reference number: A32346; MUID:88327862; PMID:2901293
A;Accession: A32346
A;Molecule type: mRNA
A;Residues: 1-33, 'H',35-41 <HE1>
A;Cross-references: UNIPARC:UPI000017376C; GB:X05111
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; T-cell; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-344/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F;23-199/Domain: extracellular #status predicted <EXT>
F;200-228/Domain: transmembrane #status predicted <TMM>
F;229-344/Domain: intracellular #status predicted <INT>
F;99,106,134/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match   7.3%; Score 130; DB 1; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0047;;
Matches   65; Conservative 51; Mismatches 112; Indels 62; Gaps 13;

```
Qy     12  YILWQLTGSAA---SGPVKELVGSVGGAVTFPLKSKVKQVDSIWTFNTTPLVTIQPEG 67
              :||:     |    |||: || |  |::| |   ::||::   ||||   |||  :|
Db     10  FLLFSLSSKGADCRDSGTVNGALGR-GINLNIPNFQMTDDIDEVRW----------ER 56
              |  :| |     |||:||  ||   | |    |     |:::| |
Qy     68  GTIIVTQNRNRERVDFPDGGY------SLKLSLKLKNDSGIYYVGIYSSSLQQPSTQEYV 121
              |   ||:|  |     |||||        |:|    | |||||  | :::   |    ||
Db     57  GSTLVAEFKRKMKPFLKSGAFEILANGDLKIKNLTRDDSGTYNVTVYSTNGTRILDKALD 116
                   |:||    ||  | |  |      |||:    ||||  || ||:|  |:|   |
Qy    122  LHVYEHLSKPKVTMGLQSNKNGTCV----TNLTCCMEHGEEDVIYTWKALGQAANESHNG 177
              |   | ||:|||   | ||| |||     ||||||||| |||:||||||||||:|||||
Db    117  LRILEMVSKPMIYWEC-SNATLTCEVLEGTDVELKLYQGKEHL----RSLRQKT------ 165
                 |   ||:|   |   |||| |||  | ||:| | | |:|      |:| |
Qy    178  SILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPL- 236
```

Db   125 FDPVPKPSIEINKTEASTDSCHLRLSC--EVKDQHVDYTWYESSGPFPKKSPGYVLDLIV 182

Qy   185 RWGESDMTFICVARNPVSRN-----FSSPI-LARK-LCEGAADDPDSSMVLLCLLLVPL 236
              : |||| ||| :|:|| |||| |||:| |||:|
Db   183 TPQNKSTFYTCQVSNPVSSKNDTVYFTLPCDLARSSGVCWTA-----TWLVVTTLIIHRI 237

Qy   237 LLS 239
          ||:
Db   238 LLT 240

RESULT 9
JH0395
biliary glycoprotein h precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0395
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0395
A;Molecule type: mRNA
A;Residues: 1-321 <KUR>
A;Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A625; GB:M69176; NID:g179434; PIDN:
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-321/Product: biliary glycoprotein h #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

Query Match   7.1%; Score 125.5; DB 2; Length 321;
Best Local Similarity 25.1%; Pred. No. 0.01;
Matches   67; Conservative   36; Mismatches   93; Indels   71; Gaps   17;

Qy   68 GTIIVTQ------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              ||||| :|: | :|| :| |:|||||||||: ||:||
Db   81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy   120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTWKALGQAANESHNGSI 179
              | || : :||||| : |:: ||| |:|| ::||||
Db   138 F--HVPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI--------NNQS 184

Qy   180 LPISWRW----GESDMTFICVAR----------NPVSRNFSSPILARKLCEG-------A 218
          ||:|| ||||||| ||||:: |: |||:|
Db   185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy   219 ADD-----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKREROEEYIEKKRVDICRETP 272
              ||| : : | ::: :|| : ||| :|:   :
Db   244 PSDTYRPGANLSLSCYAASNPPAQYSWLINGTF-----QQSTQELFI----------P 287

Qy   273 NI-CPHSGENTEY--DTIPHTNRTILK 296
          || ::|: | : ||:| : ::|
Db   288 NITVNNSGSYTCHANNSVTGCNRTTVK 314

RESULT 10
JH0396
biliary glycoprotein i precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0396
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0396
A;Molecule type: mRNA
A;Residues: 1-351 <KUR>

A;Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A626; GB:M72238; NID:g179436; PIDN
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-351/Product: biliary glycoprotein i #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

Query Match   7.1%; Score 125.5; DB 2; Length 351;
Best Local Similarity 25.1%; Pred. No. 0.011;
Matches   67; Conservative   36; Mismatches   93; Indels   71; Gaps   17;

Qy   68 GTIIVTQ------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              ||||| :|: | :|| :| |:|||||||||: ||:||
Db   81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy   120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTWKALGQAANESHNGSI 179
              | || : :||||| : |:: ||| |:|| ::||||
Db   138 F--HVPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI--------NNQS 184

Qy   180 LPISWRW----GESDMTFICVAR----------NPVSRNFSSPILARKLCEG-------A 218
          ||:|| ||||||| ||||:: |: |||:|
Db   185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy   219 ADD-----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKREROEEYIEKKRVDICRETP 272
              ||| : : | ::: :|| : ||| :|:   :
Db   244 PSDTYRPGANLSLSCYAASNPPAQYSWLINGTF-----QQSTQELFI----------P 287

Qy   273 NI-CPHSGENTEY--DTIPHTNRTILK 296
          || ::|: | : ||:| : ::|
Db   288 NITVNNSGSYTCHANNSVTGCNRTTVK 314

RESULT 11
JH0394
biliary glycoprotein g precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JH0394
R;Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A;Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones f
A;Reference number: JH0394; MUID:91222218; PMID:2025273
A;Accession: JH0394
A;Molecule type: mRNA
A;Residues: 1-417 <KUR>
A;Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A624; GB:M72238; NID:g179436; PIDN
A;Experimental source: leukocyte
C;Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C;Keywords: glycoprotein; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-383/Product: biliary glycoprotein g #status predicted <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>

Query Match   7.1%; Score 125.5; DB 2; Length 417;
Best Local Similarity 25.1%; Pred. No. 0.014;
Matches   67; Conservative   36; Mismatches   93; Indels   71; Gaps   17;

Qy   68 GTIIVTQ------NRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSL-QQPSTQE 119
              ||||| :|: | :|| :| |:|||||||||: ||:||
Db   81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy   120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTWKALGQAANESHNGSI 179
              | || : :||||| : |:: ||| |:|| ::||||
Db   138 F--HVPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI--------NNQS 184

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Qy    180  LPISWRW-----GESDMTFICVAR----------NPVSRNFSSPILARKLCEG------A  218
                |||:|       :|:||            |||||  :||||||| :|
Db    185  LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS  243

Qy    219  ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEYIEEKKRVDICRETP  272
                     ||::          :|  :|:|
Db    244  PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI----------P  287

Qy    273  NI-CPHSGENTEY--DTIPHTNRTLIK  296
                ||||           ||:|| ||||:|
Db    288  NITVNNSGSYTCHANNSVTGCNRTTVK  314
```

RESULT 12

C30127

transmembrane carcinoembryonic antigen 3 precursor - human

N;Alternate names: CD66 splice form BGPc

C;Species: Homo sapiens (man)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K

J. Cell Biol. 108, 267-276, 1989

A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs

A;Reference number: A92752; MUID:89139550; PMID:2537311

A;Accession: C30127

A;Molecule type: mRNA

A;Residues: 1-464 <BAR>

A;Cross-references: UNIPROT:Q16170; UNIPARC:UPI000072309; EMBL:X16356; EMBL:X14784

R;Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Gschmeissner, S.E.; Hajibagheri

Blood 84, 200-210, 1994

A;Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, expr

A;Reference number: I52597; MUID:9289702; PMID:8018919

A;Accession: I52597

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Cross-references: UNIPARC:UPI000072309; GB:S71326; NID:g550030; PIDN:AAB31183.1; PID:

C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

C;Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein

F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <MAT>

F;160-217/Domain: immunoglobulin homology <IMM1>

F;252-301/Domain: immunoglobulin homology <IMM2>

F;341-398/Domain: immunoglobulin homology <IMM3>

F;422-455/Domain: transmembrane #status predicted <TMM>

F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405/Bindin

Query Match   7.1%; Score 125.5; DB 2; Length 464;

Best Local Similarity 25.1%; Pred. No. 0.016;

Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

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Qy     68  GTIIVTQ------NRNRERVDFPDGGYSLKLSKLKKNDSGIYVGIYSSL-QQPSTQE  119
               :     ::|:  .:|:   |  :|:| .:::
Db     68  GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ  137

Qy    120  YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI  179
             :   :|  .:.:  .:|:
Db    138  F--HVPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI----------NNQS  184

Qy    180  LPISWRW-----GESDMTFICVAR----------NPVSRNFSSPILARKLCEG------A  218
                |||:|       :|:||            |||||  :||||||| :|
Db    185  LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS  243

Qy    219  ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEYIEEKKRVDICRETP  272
                     ||::          :|  :|:|
Db    244  PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI----------P  287

Qy    273  NI-CPHSGENTEY--DTIPHTNRTLIK  296
                ||||           ||:|| ||||:|
Db    288  NITVNNSGSYTCHANNSVTGCNRTTVK  314
```

RESULT 13

A32164

biliary glycoprotein 1 precursor, splice form a - human

N;Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane car

N;Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form a

C;Species: Homo sapiens (man)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476

R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,

Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989

A;Reference number: A32164

A;Contents: erratum

A;Accession: A32164

A;Molecule type: mRNA

A;Residues: 1-526 <HIN>

A;Cross-references: UNIPROT:P13688; UNIPARC:UPI000127483; GB:J03858; NID:g179439; PIDN

R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,

Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988

A;Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of

A;Reference number: A94206; MUID:88320555; PMID:2457922

A;Contents: annotation

A;Note: the sequence shown in this reference has been completely corrected in reference

R;Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K

J. Cell Biol. 108, 267-276, 1989

A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs

A;Reference number: A92752; MUID:89139550; PMID:2537311

A;Accession: A30127

A;Molecule type: mRNA

A;Residues: 1-526 <BAR1>

A;Cross-references: UNIPARC:UPI000127483; EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PII

A;Experimental source: splice form a

A;Accession: B30127

A;Molecule type: mRNA

A;Residues: 1-19, 'D',417-526 <BAR2>

A;Cross-references: UNIPARC:UPI0000073D2E; EMBL:X14831; NID:g37199; PIDN:CAA32940.1; PII

A;Experimental source: splice form b

R;Barnett, T.R.; Drake, L.; Pickle II, W.

Mol. Cell. Biol. 13, 1273-1282, 1993

A;Title: Human biliary glycoprotein gene: characterization of a family of novel alternat

A;Reference number: A48078; MUID:93140765; PMID:8423792

A;Accession: A48078

A;Molecule type: mRNA

A;Residues: 124-141,'H',417-526 <BAR3>

A;Cross-references: UNIPARC:UPI000173868; GB:M76742; NID:g179480; PIDN:AAA57142.1; PID:

A;Experimental source: splice form x

A;Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBIP:123606)

A;Note: neither the complete nucleic acid sequence nor the complete translation are show

R;Hauck, W.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N.

Eur. J. Biochem. 223, 529-541, 1994

A;Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami

A;Reference number: S45664; MUID:94333343; PMID:8055923

A;Accession: S45664

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-21 <HAU>

A;Cross-references: UNIPARC:UPI00006B9AC; EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PII

R;Nedellec, P.; Turbide, C.; Beauchemin, N.

Eur. J. Biochem. 231, 104-114, 1995

A;Title: Characterization and transcriptional activity of the mouse biliary glycoprotein

A;Reference number: S65939; MUID:95354678; PMID:7628460

A;Accession: S65939

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-21 <NED>

A;Cross-references: UNIPARC:UPI00006B9AC; EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PII

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

A;Note: only a part of the coding sequence is given

R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.

Genomics 14, 384-390, 1992

A;Title: Identification of three new genes and estimation of the size of the carcinoembr

A;Reference number: A44476; MUID:93052339; PMID:1427854

A;Contents: annotation; alignment of related sequences

C;Genetics:

A;Gene: GDB:BGP
A;Cross-references: GDB:127992; OMIM:109770
A;Map position: 19q13.2-19q13.2
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;35-526/Product: signal sequence #status predicted <SIG>
F;35-526/Product: biliary glycoprotein 1, splice form a #status predicted <MATA>
F;35-141/Domain: extracellular #status predicted <EXT>
F;35-319,'D',417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M
F;35-141,'H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted <M
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>
F;341-398/Domain: immunoglobulin homology <IMM3>
F;425-454/Domain: transmembrane #status predicted <TMM>
F;453-526/Domain: intracellular #status Predicted <INT>
F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/Bi

Query Match   7.1%;   Score 125.5;   DB 1;   Length 526;
Best Local Similarity   25.1%;   Pred. No. 0.018;
Matches   67;   Conservative   36;   Mismatches   93;   Indels   71;   Gaps   17;

Qy   68 GTIIVTQ------NRNRERVDFPDGGVSLKKLSKLKKNDSGIYVVGIYSSSL-QQPSTQE 119
                                                                   ||||||||
Db   81 GYAIGTQQATPGPANSGRETI-YPNA--SLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQ 137

Qy   120 YVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSI 179
                 :| ||| | | | | : |:   :|
Db   138 F--HVYPELPKPSISSNNSNPVEDKDAVAFTC--EPETQDTTYLWWI-------NNQS 184

Qy   180 LPISWRW----GESDMTFICVAR---------NPVSRNFSSPILARKLCEG------A 218
                 ||:|| | | ::||| |||| | |
Db   185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243

Qy   219 ADD----PDSSMVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP 272
                 ||| :|: |||| | |:|| |:
Db   244 PSDTYYRPGANLSLSCYAASNPPAQYSWLINGTF----QQSTQELFI---------P 287

Qy   273 NI-CPHSGENTEY--DTIPHTNRTILK 296
                 || :| ||| ::|| |||
Db   288 NITVNNSGSYTCHANNSVTGCNRTTVK 314

RESULT 14
A27681
nonspecific cross-reacting antigen precursor - human
N;Alternate names: NCA; TEX/NCA
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R;Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A;Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
A;Reference number: A26902; MUID:87298464; PMID:3619891
A;Accession: A26902
A;Molecule type: DNA
A;Residues: 1-141 <OIK>
A;Cross-references: UNIPROT:Q13774; UNIPARC:UPI000000072416; NID:g180230; PIDN:
R;Thompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, C
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
A;Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami
A;Reference number: A29875; MUID:87204248; PMID:3033672
A;Accession: A29875
A;Molecule type: DNA
A;Residues: 23-141 <THO>
A;Cross-references: UNIPARC:UPI0000177070; GB:M16337
A;Note: the authors translated the codon ACT for residue 64 as Tyr
R;Tawaragi, Y.; Oikawa, S.; Matsuoka, Y.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 150, 89-96, 1988
A;Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carci
A;Reference number: A27681; MUID:88106638; PMID:3337731
A;Accession: A27681
A;Molecule type: mRNA

A;Residues: 1-238,'V',240-344 <TAW>
A;Cross-references: UNIPARC:UPI000012748C; GB:M18728; NID:g189084; PIDN:AAA59907.1; PID
R;Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A;Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and
A;Reference number: A31037; MUID:89122014; PMID:3220478
A;Accession: B31037
A;Molecule type: mRNA
A;Residues: 1-137,'L',139-344 <BAR>
A;Cross-references: UNIPARC:UPI00016ADC6; GB:M29541; NID:g189103; PIDN:AAA59915.1; PID
R;Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A;Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (N
A;Reference number: A29918; MUID:88139389; PMID:2830274
A;Accession: A29918
A;Molecule type: mRNA
A;Residues: 1-344 <NEU>
A;Cross-references: UNIPARC:UPI000006DF42; GB:M18216; GB:J03550; NID:g178690; PIDN:AAA5
R;Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwaibold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and in
A;Reference number: A27709; MUID:88268882; PMID:3390172
A;Accession: A27709
A;Molecule type: protein
A;Residues: 35-95,99-120,123-138,149-151,'X',153-162,166,'X',168-172,'X',174-193,221-23
A;Cross-references: UNIPARC:UPI0000177071; UNIPARC:UPI0000177072; UNIPARC:UPI0000177073
078;UNIPARC:UPI0000177079; UNIPARC:UPI0000177007A
R;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspec
A;Reference number: A36271; MUID:90256782; PMID:2341397
A;Accession: A36271
A;Molecule type: protein
A;Residues: 35-42,44-53,55-80,83-134,139-160,166-172,174-180,191-194,204-224,233-308,31
A;Cross-references: UNIPARC:UPI0000177007B; UNIPARC:UPI0000177007C; UNIPARC:UPI0000177007D
082; UNIPARC:UPI0000177083; UNIPARC:UPI0000177084
R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A;Reference number: A26414; MUID:87147209; PMID:3469650
A;Accession: C26414
A;Molecule type: protein
A;Residues: 35-69 <PAX>
A;Cross-references: UNIPARC:UPI0000177085
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoemb
A;Reference number: A44476; MUID:93052339; PMID:1427854
A;Accession: E44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
A;Cross-references: UNIPARC:UPI0000177086
A;Accession: F44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-137,'L',139-141 <KH2>
A;Cross-references: UNIPARC:UPI0000177086
C;Comment: This protein appears to be processed at the carboxyl terminus and anchored t
C;Genetics:
A;Gene: GDB:NCA
A;Cross-references: GDB:120221; OMIM:163980
A;Map position: 19q13.2-19q13.2
A;Introns: 22/1
A;Note: the list of introns may be incomplete
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;252-301/Domain: immunoglobulin homology <IMM2>

F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalent
F;309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

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Query Match             7.0%;  Score 124.5; DB 2;  Length 344;
Best Local Similarity  22.4%;  Pred. No. 0.013;
Matches   75;  Conservative  35;  Mismatches  118;  Indels  107;  Gaps  16;

Qy    53 WTFNTTPLVTIQ------PEGGTII-----VTQNR-----NRERVD----------- 82
            |||:|                 :|:|           ||||
Db    28 WNPPTTAKLTIESTPFNVAEGKEVLLLAHNLPQNRIGYSWYKGERVDGNSLIVGVVIGTQ 87

Qy    83 --FPDGGY---------SLKLSKLKKNDSGIYYVGIYSSL-QQPSTQEVLVHVYEHLS 129
            |  |              :||:|:|||::|:|  | ||:::::    ||
Db    88 QATPGPAYSGRETIYPNASLLIQNVTQNDTGFYTLQVIKSDLVNEEATGQF--HVYPELP 145

Qy   130 KPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW--- 186
            |:   |||:|:|||||||:|||||||||||||||||:||||||||:||:||||:||||
Db   146 KPSISSNSNPVEDKDAVAFTC--EPEVQNTTYLWMV-----------NGQSLPVSPRLQLS 194

Qy   187 -GESDMTFI-----------CVARNPVSRNFSSPILARKLC---------EGAADDPDSS 225
             |::|||                  |:||||| |:||| |            ||||||||
Db   195 NGNMTLTLLSVKRNDAGSYECEIQNPASANRSDPVTLNVLYGPDGPTISPSKANYRPGEN 254

Qy   226 MVLLCLLL--VPLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETPNI-------- 274
             : :|:|              :| |            ||::|||
Db   255 LNLSCHAASNPPAQYSWFINGTF----QQSTQELFI---------------PNITVNNSGSYM 298

Qy   275 CPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEI 309
             |  :||:|  :|||:|||:|||||||| ||:||
Db   299 CQAHNSATGLNRTTVTMITVSGSAPVLSAVATVGI 333
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RESULT 15
S34338
biliary glycoprotein F - mouse
N;Alternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S34338; JC1510; A41093
R;Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
submitted to the EMBL Data Library, July 1992
A;Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A;Reference number: S34338
A;Accession: S34338
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-521 <HUA>
A;Cross-references: UNIPROT:Q61352; UNIPARC:UPI0000283F8; EMBL:X67281; NID:g312585; PII
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprc
A;Reference number: JC1505; MUID:9273228; PMID:8500759
A;Accession: JC1510
A;Molecule type: mRNA
A;Residues: 1-81,'Q',83-141,'P',143-521 <MCC>
A;Cross-references: UNIPARC:UPI000177068; GB:X67281
R;Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A;Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen
A;Reference number: A41093; MUID:9128B498; PMID:1648219
A;Accession: A41093
A;Status: preliminary
A;Molecule type: protein
A;Residues: 35-59 <WIL>
A;Cross-references: UNIPARC:UPI0000177069
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
C;Genetics:
A;Gene: BgpF
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (

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Query Match             6.9%;  Score 122.5; DB 2;  Length 521;
Best Local Similarity  22.4%;  Pred. No. 0.032;
Matches   47;  Conservative  32;  Mismatches  70;  Indels  61;  Gaps  8;

Qy    53 WTFNTTPLVTIQ------PEGGTIIVTQN-----------RNRERVDFPDG-- 86
            |||:|                 :|:|              :|::
Db    28 WSPPTTAEVTIEAVPPQVAEDNNVLLLVHNLPLALGAFAWYKGNPVSTNABIVHFVTGTN 87

Qy    87 ----------GYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYV-LHVYEHLS 129
              |||:|:|||:::||   | ||
Db    88 KTTTGPAHSGRETVYSNGSLLIQRVTVKDTGVYTIEMTDENFRR--TEATVQFHVHQLLL 145

Qy   130 KPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGES 189
            ||||||||||||||||||||||||||||||||||||||||||||||||||:||||:||
Db   146 KPNITSNNSNPVEGDDSVSLTCDSYTDPDNITYLWSRNGESLSE---GDRLKLS--EGNR 200

Qy   190 DMT------------FICVARNPVSRNFSSP 208
             ||              :|:     ||||||
Db   201 TLTLNVTRNDTGPYVCETRNPVSVNRSDP 230
```

Search completed: March 29, 2007, 02:28:20
Job time : 68 secs

GenCore version 6.2
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OM protein - protein search, using sw model

Run on: March 29, 2007, 02:27:44 ; Search time 349 Seconds
(without alignments)
1029.117 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTLIYILIWQLTGS.........PHSLLTMPDTPRLFAYENVI 335

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	1772	100.0	335	1	SLAF7_HUMAN	Q9nq25 homo sapien
2	822	46.4	333	2	Q3T9A2_MOUSE	Q3t9a2 mus musculu
3	815	46.0	333	1	SLAF7_MOUSE	Q8bhk6 mus musculu
4	778.5	43.9	335	2	Q18PI2_MOUSE	Q18pi2 mus musculu
5	658	37.1	300	2	Q18PG4_MOUSE	Q18pg4 mus musculu
6	368	20.8	328	2	Q3TBT1_MOUSE	Q3tbt1 mus musculu
7	364.5	20.6	329	2	Q18PI6_MOUSE	Q18pi6 mus musculu
8	362.5	20.5	328	1	O15430_HUMAN	O15430 homo sapien
9	362.5	20.5	329	2	Q92178_MOUSE	Q92178 mus musculu
10	360.5	20.3	329	2	Q18PI7_MOUSE	Q18pi7 mus musculu
11	359	20.3	339	2	Q8WWI8_HUMAN	Q8wwi8 homo sapien
12	358.5	20.3	645	2	Q6NZB6_MOUSE	Q6nzb6 mus musculu
13	358	20.2	345	2	Q9UIB8_HUMAN	Q9uib8 homo sapien
14	354.5	20.0	328	2	Q6FHA8_HUMAN	Q6fha8 homo sapien
15	354.5	20.0	649	2	Q7TMP7_MOUSE	Q7tmp7 mus musculu
16	354.5	20.0	654	1	LY9_MOUSE	Q01965 mus musculu
17	353.5	19.9	544	2	Q8C2D4_MOUSE	Q8c2d4 mus musculu
18	353.5	19.9	654	2	Q4VBG4_MOUSE	Q4vbg4 mus musculu
19	330.5	18.7	289	1	SLAF9_HUMAN	Q96a28 homo sapien
20	329	18.6	539	2	Q8C9E4_MOUSE	Q8c9e4 mus musculu
21	318	17.9	655	1	LY9_HUMAN	Q9hbg7 homo sapien
22	315.5	17.8	331	1	SLAF6_HUMAN	Q96du3 homo sapien
23	311	17.6	332	1	Q5TAS4_HUMAN	Q5tas4 homo sapien
24	311	17.6	602	2	Q5VYH7_HUMAN	Q5vyh7 homo sapien
25	308	17.4	280	2	O95660_HUMAN	O95660 homo sapien
26	307.5	17.4	285	1	SLAF9_MOUSE	Q9d780 mus musculu
27	307.5	17.4	285	2	Q18PH4_MOUSE	Q18ph4 mus musculu
28	307.5	17.4	285	2	Q18PH6_MOUSE	Q18ph6 mus musculu
29	304	17.2	272	2	Q9UIB7_HUMAN	Q9uib7 homo sapien
30	290.5	16.4	241	2	Q9UIB6_HUMAN	Q9uib6 homo sapien
31	282.5	15.9	526	2	Q5VYH9_HUMAN	Q5vyh9 homo sapien
32	281	15.9	197	2	Q9UIT7_HUMAN	Q9uit7 homo sapien
33	260	14.7	271	2	Q5BKU7_HUMAN	Q5bku7 homo sapien
34	254	14.3	334	2	Q3SZI9_BOVIN	Q3szi9 bos taurus
35	250.5	14.1	214	2	Q5H9R1_HUMAN	Q5h9r1 homo sapien
36	238.5	13.5	424	2	Q5VYH8_HUMAN	Q5vyh8 homo sapien
37	226.5	12.8	351	2	Q18PJ2_MOUSE	Q18pj2 mus musculu
38	225.5	12.7	331	2	Q18PG5_MOUSE	Q18pg5 mus musculu
39	225.5	12.7	351	1	SLAF6_MOUSE	Q9et39 mus musculu
40	225.5	12.7	351	2	Q18PJ0_MOUSE	Q18pj0 mus musculu
41	214	12.1	167	2	Q5RBI0_PONPY	Q5rbi0 pongo pygma
42	213.5	12.0	270	2	Q5VYI1_HUMAN	Q5vyi1 homo sapien
43	204.5	11.5	338	2	Q95MM6_BOVIN	Q95mm6 bos taurus
44	200.5	11.3	338	2	Q1RML5_BOVIN	Q1rml5 bos taurus
45	199.5	11.3	221	2	Q5TAS6_HUMAN	Q5tas6 homo sapien
46	197.5	11.1	338	2	Q28317_BOSIN	Q28317 bos indicus
47	196	11.1	338	2	Q28318_SHEEP	Q28318 ovis aries
48	196	11.1	338	2	Q283L5_CAPHI	Q283l5 capra hircu
49	193.5	10.9	338	2	Q283L6_BUBBU	Q283l6 bubalus bub
50	188.5	10.6	343	2	Q18PK4_MOUSE	Q18pk4 mus musculu
51	187.5	10.6	336	2	Q9GJT3_SAGOE	Q9gjt3 saguinus oe
52	186	10.5	343	1	SLAF1_MOUSE	Q9qum4 mus musculu
53	186	10.5	343	1	Q544K1_MOUSE	Q544k1 m adult mal
54	183.5	10.4	335	2	Q96QR3_HUMAN	Q96qr3 homo sapien
55	183	10.3	266	2	Q9CUC8_MOUSE	Q9cuc8 mus musculu
56	183	10.3	343	2	Q3TA28_MOUSE	Q3ta28 mus musculu
57	182.5	10.3	335	1	SLAF1_HUMAN	Q13291 homo sapien
58	182.5	10.1	335	2	Q5W172_HUMAN	Q5w172 homo sapien
59	179	10.1	278	2	Q3UQA2_MOUSE	Q3uqa2 mus musculu
60	178	10.0	278	2	SLAF8_MOUSE	Q9d3g2 mus musculu
61	177	10.0	278	2	Q3U1C3_MOUSE	Q3u1c3 mus musculu
62	177	10.0	278	2	Q18PH1_MOUSE	Q18ph1 mus musculu
63	171	9.7	329	2	Q5VYI5_HUMAN	Q5vyi5 homo sapien
64	170	9.6	365	2	Q5VYI2_HUMAN	Q5vyi2 homo sapien
65	167.5	9.5	342	1	SLAF1_CANFA	Q95mm9 canis famil
66	163.5	9.2	370	1	CD244_HUMAN	Q9bzw8 homo sapien
67	163.5	9.2	370	2	Q5VYI7_HUMAN	Q5vyi7 homo sapien
68	160.5	9.1	338	2	Q5M893_BOVIN	Q5m893 bos taurus
69	159.5	9.0	329	2	Q5M7A8_XENLA	Q5m7a8 xenopus lae
70	158.5	8.9	326	1	SLAF8_HUMAN	Q8cau4 mus musculu
71	150.5	8.5	285	1	Q32MC6_HUMAN	Q9p0v8 homo sapien
72	150.5	8.5	285	2	Q8N7I3_HUMAN	Q32mc6 homo sapien
73	145.5	8.2	416	2	Q67IP8_HUMAN	Q8n7i3 homo sapien
74	145.5	8.2	416	2	Q62R17_HUMAN	Q67ip8 homo sapien
75	145	8.2	211	2	CD2_MOUSE	Q62r17 homo sapien
76	144	8.1	344	1	Q5SRC1_MOUSE	P08920 mus musculu
77	144	8.1	344	2	Q9R201_MOUSE	Q5src1 mus musculu
78	144	8.1	344	2	Q9HBE9_HUMAN	Q9r201 mus musculu
79	142	8.0	207	2	Q62WL4_HUMAN	Q9hbe9 homo sapien
80	142	8.0	367	2	Q5BKG7_XENTR	Q62wl4 homo sapien
81	141	8.0	291	2	Q4SQQ1_TETNG	Q5bkg7 xenopus tro
82	139	7.8	347	2	Q764N3_PIG	Q4sqq1 tetraodon n
83	138.5	7.8	340	2	Q640R3_MOUSE	Q764n3 sus scrofa
84	138.5	7.8	413	2	Q6SZ63_PANTR	Q640r3 mus musculu
85	137.5	7.8	345	2	Q53F96_HUMAN	Q6sz63 pan troglod
86	136.5	7.7	351	2	Q2ABP7_EPTBU	Q53f96 homo sapien
87	136	7.7	368	1	Q6QX36_MOUSE	Q2abp7 eptatretus
88	135.5	7.6	289	2	Q4S0F0_TETNG	Q6qx36 m crkd-bind
89	135	7.6	302	2	CD48_RAT	Q4s0f0 tetraodon n
90	134	7.6	240	1	Q2ABP8_EPTBU	P10252 rattus norv
91	134	7.6	370	2	CD2_HUMAN	Q2abp8 eptatretus
92	133.5	7.6	351	1	Q9EQK9_RAT	P06729 rattus norv
93	133.5	7.5	394	2	Q502A9_BRARE	Q9eqk9 rattus norv
94	133	7.5	422	2	CXAR_BRARE	Q502a9 brachydanio
95	132.5	7.5	372	1	Q5IOM6_RAT	Q90y50 brachydanio
96	131	7.4	344	2	Q5R9N6_PONPY	Q5iom6 rattus norv
97	131	7.4	525	2	Q58DG9_BOVIN	Q5r9n6 pongo pygma
98	130	7.3	249	2	CD2_RAT	Q58dg9 bos taurus
99	130	7.3	344	1	Q28753_9CETA	P08921 rattus norv
100	128.5	7.3	253	2	Q6P2J4_HUMAN	Q28753 ovis sp. lf
101	128	7.2	193	2	Q3UK50_MOUSE	Q6p2j4 homo sapien
102	127.5	7.2	240	2	CD48_MOUSE	Q3uk50 mus musculu
103	126.5	7.1	240	2	CD48_MOUSE	P18181 mus musculu
104	126.5	7.1	240	2	Q6P905_MOUSE	Q6p905 mus musculu

Index	Score	Score	Name	Num	Length	Accession	Species
105	126	7.1	Q4T2U2_TETNG	2	318	Q4t2u2	tetraodon n
106	125.5	7.1	Q18PH8_HUMAN	2	240	Q18ph8	mus musculu
107	125.5	7.1	Q5UB49_HUMAN	2	368	Q5ub49	homo sapien
108	125.5	7.1	Q16170_HUMAN	2	464	Q16170	homo sapien
109	125.5	7.1	Q96CA7_HUMAN	2	468	Q96ca7	homo sapien
110	125.5	7.1	Q3KRG8_HUMAN	2	493	Q3krg8	homo sapien
111	125.5	7.1	CEAM1_HUMAN	2	526	Ceam1	homo sapien
112	125	7.1	Q6SZ62_PAPAN	2	344	Q6sz62	papio anubi
113	125	7.1	Q7KYP5_HUMAN	2	373	Q7kyp5	homo sapien
114	124.5	7.0	CEAM6_HUMAN	1	344	P40199	homo sapien
115	124.5	7.0	Q53XP7_HUMAN	2	344	Q53xp7	homo sapien
116	124.5	7.0	Q13774_HUMAN	2	344	Q13774	homo sapien
117	124.5	7.0	Q13854_HUMAN	2	461	Q13854	homo sapien
118	124	7.0	Q6SZ58_MACAS	2	345	Q6sz58	macaca assa
119	123.5	7.0	Q28754_9CETA	2	227	Q28754	ovis sp. lf
120	123	7.0	Q8BFV0_MOUSE	2	140	Q8bfv0	m 16 days n
121	123	6.9	CD244_RAT	1	311	Q9jlm2	rattus norv
122	122.5	6.9	Q61351_MOUSE	2	458	Q61351	mus musculu
123	122.5	6.9	Q61352_MOUSE	2	521	Q61352	mus musculu
124	122	6.9	Q9N166_PAPHA	2	326	Q9n166	papio hamad
125	122	6.9	Q6SZ56_MACNE	2	334	Q6sz56	macaca neme
126	122	6.9	Q6SZ57_MACAR	2	341	Q6sz57	macaca arct
127	121.5	6.9	Q80V04_MOUSE	2	377	Q80v04	mus musculu
128	121.5	6.9	Q8BJE2_MOUSE	2	536	Q8bje2	mus musculu
129	121	6.9	Q3U0A2_MOUSE	2	140	Q3u0a2	m activated
130	121	6.8	CD2_MACFA	1	351	Q68z61	macaca fasc
131	119.5	6.7	Q9IB08_9PERC	2	332	Q9ib08	sphaeroides
132	119.5	6.7	CXAR_HUMAN	1	365	P78310	homo sapien
133	119.5	6.7	CXAR_PONPY	1	365	Q5r764	pongo pygma
134	118.5	6.7	Q925P2_MOUSE	2	520	Q925p2	mus musculu
135	118	6.7	Q2KH26_BOVIN	2	347	Q2kh26	bos taurus
136	118	6.7	Q5XGG4_XENTR	2	347	Q5xgg4	xenopus tro
137	118	6.7	Q28D52_XENTR	2	366	Q28d52	xenopus tro
138	116.5	6.6	GPA33_HUMAN	1	319	Q99795	homo sapien
139	116.5	6.6	Q5VZP6_HUMAN	2	319	Q5vzp6	homo sapien
140	116.5	6.6	Q17G58_AEDAE	2	334	Q17g58	aedes aegyp
141	116.5	6.6	Q6SZ59_CERTO	2	350	Q6sz59	cercocebus
142	115	6.5	Q6SZ60_MACMU	2	342	Q6sz60	macaca mula
143	115	6.5	Q90ZL5_ANAPL	2	357	Q90zl5	anas platyr
144	115	6.5	Q8N4F1_HUMAN	2	430	Q8n4f1	homo sapien
145	114.5	6.5	CEAM5_HUMAN	1	702	P06731	homo sapien
146	114.5	6.5	Q53G30_HUMAN	2	702	Q53g30	homo sapien
147	114.5	6.5	Q8N4D0_HUMAN	2	702	Q8n4d0	homo sapien
148	114	6.4	Q4SPD7_TETNG	2	239	Q4spd7	tetraodon n
149	114	6.4	Q3LFS7_MOUSE	2	236	Q31fs7	mus musculu
150	113.5	6.4	Q3LFS5_MOUSE	2	450	Q31fs5	mus musculu
151	113.5	6.4	Q91W54_MOUSE	2	454	Q91w54	mus musculu
152	113.5	6.4	CEAM1_MOUSE	1	521	P31809	mus musculu
153	113.5	6.4	Q925P3_MOUSE	2	521	Q925p3	mus musculu
154	113	6.4	Q9H6B4_HUMAN	2	373	Q9h6b4	homo sapien
155	113	6.4	Q811T7_MOUSE	2	621	Q811t7	mus musculu
156	112.5	6.3	VSIG2_MOUSE	1	328	Q9z109	mus musculu
157	111.5	6.3	Q2ABQ0_EPTBU	2	357	Q2abq0	eptatretus
158	111.5	6.3	Q5DX21_HUMAN	2	431	Q5dx21	homo sapien
159	111	6.3	Q8K1G0_RAT	2	372	Q8k1g0	rattus norv
160	111	6.2	Q29RR6_BOVIN	2	382	Q29rr6	bos taurus
161	110.5	6.2	Q3ZCC6_BOVIN	2	319	Q3zcc6	bos taurus
162	110.5	6.2	CD4_CANFA	1	463	P33705	canis famil
163	110.5	6.2	Q4VWT2_9PIPI	2	466	Q4vwt2	xenopus sp.
164	110	6.2	Q8HXQ6_PIG	2	539	Q8hxq6	sus scrofa
165	109.5	6.2	Q6LBK1_CANFA	2	432	Q61bk1	canis famil
166	109	6.1	CD276_MOUSE	1	316	Q8ve98	mus musculu
167	108.5	6.1	CXAR_BOVIN	1	365	Q8wmv3	bos taurus
168	108.5	6.1	Q3SZH9_BOVIN	2	365	Q3szh9	bos taurus
169	108	6.1	CD276_RAT	1	316	Q7tpb4	rattus norv
170	107.5	6.1	Q1LXQ8_BRARE	2	229	Q11xq8	brachydanio
171	107	6.0	Q7QJG1_ANOGA	2	349	Q7qjg1	anopheles g
172	107	6.0	Q9ESE5_MOUSE	2	399	Q9ese5	mus musculu
173	106.5	6.0	Q9XYS4_HYDAT	2	752	Q9xys4	hydra atten
174	106.5	6.0	Q8IIY3_PLAF7	2	4138	Q8iiy3	plasmodium
175	106	6.0	Q3UV86_MOUSE	2	397	Q3uv86	mus musculu
176	106	6.0	Q9SJY2_ARATH	2	897	Q9sjy2	arabidopsis
177	105.5	6.0	Q6FHB1_HUMAN	2	323	Q6fhb1	homo sapien
178	105.5	6.0	CD86_HUMAN	1	329	P42081	homo sapien
179	105.5	6.0	Q6GTS4_HUMAN	2	329	Q6gts4	homo sapien
180	105.5	6.0	Q9PWR4_CHICK	2	335	Q9pwr4	gallus gall
181	105	6.0	Q9JIE1_MOUSE	2	398	Q9jie1	mus musculu
182	105	5.9	Q566N1_BRARE	2	245	Q566n1	brachydanio
183	105	5.9	Q3TAZ6_MOUSE	2	312	Q3taz6	mus musculu
184	105	5.9	CD244_MOUSE	1	397	Q07763	mus musculu
185	104.5	5.9	Q9TU79_PIG	2	319	Q9tu79	sus scrofa
186	104.5	5.9	Q8A321_BACTN	2	1271	Q8a321	bacteroides
187	104.5	5.9	Q50SS7_ENTHI	2	1656	Q50ss7	entamoeba h
188	104	5.9	Q920L8_MOUSE	2	455	Q92018	mus musculu
189	104	5.9	Q9EQT7_MOUSE	2	535	Q9eqt7	mus musculu
190	104	5.9	Q94191_PARBR	2	1220	Q94191	paracoccidi
191	103.5	5.8	Q9TU80_CANFA	2	319	Q9tu80	canis famil
192	103.5	5.8	Q9BDB8_CERTO	2	323	Q9bdb8	cercocebus
193	103.5	5.8	Q8R373_MOUSE	2	373	Q8r373	mus musculu
194	103.5	5.8	Q8N7T8_HUMAN	2	406	Q8n7t8	homo sapien
195	103	5.8	Q8AXC7_FUGRU	2	1062	Q8axc7	fugu rubrip
196	103	5.8	Q8AXC8_FUGRU	2	1078	Q8axc8	fugu rubrip
197	103	5.8	Q7KQT5_DROME	2	1479	Q7kqt5	drosophila
198	102.5	5.8	Q8JSP1_ASF	2	304	Q8jsp1	african swi
199	102.5	5.8	Q9BDM4_MACMU	2	323	Q9bdm4	macaca mula
200	102.5	5.8	Q9YGH1_CHICK	2	335	Q9ygh1	gallus gall
201	102.5	5.8	Q4KLE4_XENLA	2	359	Q4kle4	xenopus lae
202	102.5	5.8	Q92OS5_MOUSE	2	373	Q92os5	mus musculu
203	102.5	5.8	CEAM1_RAT	1	519	P16573	rattus norv
204	102.5	5.8	MET_MICMU	1	1382	Q9q189	microcebus
205	102	5.8	Q9V4Y0_DROME	2	1482	Q9v4y0	drosophila
206	101.5	5.7	Q3TDI8_MOUSE	2	341	Q3tdi8	mus musculu
207	101.5	5.7	Q3TBIO_MOUSE	2	398	Q3tbio	mus musculu
208	101.5	5.7	O22271_ARATH	2	761	O22271	arabidopsis
209	101	5.7	Q2YHT7_CHICK	2	300	Q2yht7	gallus gall
210	101	5.7	Q4SQP9_TETNG	2	324	Q4sqp9	tetraodon n
211	101	5.7	CEAM8_HUMAN	1	349	P31997	homo sapien
212	101	5.7	LACH_SCHAM	1	349	Q26474	schistocerc
213	101	5.7	Q6VAN5_BOVIN	2	365	Q6van5	bos taurus
214	101	5.7	Q6VAN6_BOVIN	2	372	Q6van6	bos taurus
215	101	5.7	Q6VAN7_BOVIN	2	429	Q6van7	bos taurus
216	101	5.7	Q6DDE7_XENLA	2	432	Q6dde7	xenopus lae
217	101	5.7	Q6VAN8_BOVIN	2	436	Q6van8	bos taurus
218	101	5.7	Q2TB54_MOUSE	2	535	Q2tb54	mus musculu
219	101	5.7	CD166_CHICK	1	588	P42292	gallus gall
220	100.5	5.7	Q17EB4_AEDAE	2	1262	Q17eb4	aedes aegyp
221	100.5	5.7	Q6L0Y1_PICTO	2	1637	Q610y1	picrophilus
222	100.5	5.7	Q9CFA4_LACLA	2	259	Q9cfa4	lactococcus
223	100.5	5.7	Q8UWL2_ICTPU	2	280	Q8uwl2	ictalurus p
224	100.5	5.7	Q9BDM2_CERAE	2	323	Q9bdm2	cercopithec
225	100.5	5.7	Q4RRT9_TETNG	2	540	Q4rrt9	tetraodon n
226	100.5	5.7	CD166_CARAU	1	555	Q90304	carassius a
227	100.5	5.7	Q17CF5_AEDAE	2	1410	Q17cf5	aedes aegyp
228	100	5.6	Q6JHT1_ASF	2	324	Q6jht1	african swi
229	100	5.6	Q31KY5_SYNP7	2	452	Q31ky5	synechococc
230	99.5	5.6	Q5SNP8_BRARE	2	318	Q5snp8	brachydanio
231	99.5	5.6	Q9BDM9_MACNE	2	323	Q9bdm9	macaca neme
232	99.5	5.6	Q9YGV5_CHICK	2	335	Q9ygv5	gallus gall
233	99.5	5.6	Q75JX6_DICDI	2	658	Q75jx6	dictyosteli
234	99.5	5.6	Q559P5_DICDI	2	693	Q559p5	dictyosteli
235	99.5	5.6	MET_OTOGA	1	1382	Q2qlh6	otolemur ga
236	99.5	5.6	Q4RJ20_TETNG	2	3493	Q4rj20	tetraodon n
237	99	5.6	PVR_CERAE	1	417	P32506	cercopithec
238	99	5.6	Q2TB55_MOUSE	2	591	Q2tb55	mus musculu
239	98.5	5.6	Q8BNV8_MOUSE	2	229	Q8bnv8	mus musculu
240	98.5	5.6	Q16W85_AEDAE	2	368	Q16w85	aedes aegyp
241	98.5	5.6	UE1D1_HUMAN	2	404	Q9gzz9	homo sapien
242	98.5	5.6	Q3V5D4_XENLA	2	409	Q3v5d4	xenopus lae
243	98.5	5.6	Q410H3_KINRA	2	495	Q410h3	kineococcus
244	98.5	5.6	BT1A1_BOVIN	2	526	P18892	bos taurus
245	98.5	5.6	Q8SQ83_TRIVU	2	733	Q8sq83	trichosurus
246	98.5	5.6	Q3ZVM1_SPICI	2	840	Q3zvm1	spiroplasma
247	98.5	5.6	Q21038_CAEEL	2	1227	Q21038	caenorhabdi
248	98.5	5.6	Q2IBC7_RAT	2	1382	Q2ibc7	rattus norv
249	98	5.5	CD2_HORSE	1	347	P37998	equus cabal
250	98	5.5	Q6BE00_XENLA	2	484	Q6be00	xenopus lae

No.	%	Score	Len	N	Name	Accession	Species
251	98	5.5	503	1	SHP51_HUMAN	P78324	h tyrosine-
252	98	5.5	581	2	Q4SFC6_TETNG	Q4sfc6	tetraodon n
253	98	5.5	1209	2	Q4SF88_TETNG	Q4sf88	tetraodon n
254	98	5.5	1382	1	MET_RAT	P97523	rattus norv
255	97.5	5.5	428	2	Q5U2P2_RAT	Q5u2p2	rattus norv
256	97.5	5.5	474	2	Q70815_ANOGA	Q7q815	anopheles g
257	97.5	5.5	562	2	Q6YNR7_BRARE	Q6ynr7	brachydanio
258	97.5	5.5	591	2	Q6NP04_DROME	Q6np04	drosophila
259	97.5	5.5	1382	2	Q2IBG7_EULMM	Q2ibg7	eulemur mac
260	97.5	5.5	2772	2	Q9VAV4_DROME	Q9vav4	drosophila
261	97.5	5.5	2776	2	Q869A0_DROME	Q869a0	drosophila
262	97.5	5.5	2894	2	Q7KRX2_DROME	Q7krx2	drosophila
263	97.5	5.5	2898	2	Q868Z9_DROME	Q868z9	drosophila
264	97	5.5	452	2	Q5NOY6_SYNP6	Q5n0y6	synechococc
265	97	5.5	484	2	Q26475_SCHAM	Q26475	schistocerc
266	97	5.5	773	1	PIGR_RABIT	P01832	oryctolagus
267	96.5	5.4	311	2	Q1QPC5_BOVIN	Q1qpc5	bos taurus
268	96.5	5.4	347	2	Q60HI1_EPTBU	Q60hi1	eptatretus
269	96.5	5.4	358	2	Q1T2T1_MEDTR	Q1t2t1	medicago tr
270	96.5	5.4	368	2	Q6RWT3_BOVIN	Q6rwt3	bos taurus
271	96.5	5.4	375	2	Q6RWT4_BOVIN	Q6rwt4	bos taurus
272	96.5	5.4	402	2	Q89501_ASF	Q89501	african swi
273	96.5	5.4	402	2	Q4TZL0_ASF	Q4tzl0	african swi
274	96.5	5.4	432	2	Q6RWT5_BOVIN	Q6rwt5	bos taurus
275	96.5	5.4	439	2	Q6RWT6_BOVIN	Q6rwt6	bos taurus
276	96.5	5.4	534	1	CD276_HUMAN	Q5zpr3	homo sapien
277	96.5	5.4	866	2	Q2QLD2_CARPS	Q2qld2	carollia pe
278	96.5	5.4	1381	2	Q2IBA6_CERAE	Q2iba6	cercopithec
279	96.5	5.4	1896	2	Q91AJ1_XENLA	Q91aj1	xenopus lae
280	96	5.4	339	2	Q91AZ7_9PERC	Q91az7	sphoeroides
281	96	5.4	341	2	Q61354_MOUSE	Q61354	mus musculu
282	96	5.4	359	1	LACH_DROME	Q24372	drosophila
283	96	5.4	375	2	Q43E40_9CHLB	Q43e40	chlorobium
284	96	5.4	457	2	Q4BKK5_BURVI	Q4bkk5	burkholderi
285	96	5.4	484	2	Q5QSL1_XENTR	Q5qsl1	xenopus tro
286	96	5.4	494	2	Q4VAN1_HUMAN	Q4van1	homo sapien
287	96	5.4	526	1	BT1A1_HUMAN	Q13410	homo sapien
288	96	5.4	526	2	Q4VAN2_HUMAN	Q4van2	homo sapien
289	96	5.4	526	2	Q4VAN3_HUMAN	Q4van3	homo sapien
290	96	5.4	1087	1	PGFRA_XENLA	P26619	xenopus lae
291	95.5	5.4	1451	2	MYOM1_HUMAN	P52179	homo sapien
292	95.5	5.4	1685	2	Q6ZUU0_HUMAN	Q6zuu0	homo sapien
293	95.5	5.4	1685	2	Q9JHL6_RAT	Q9jhl6	rattus norv
294	95.5	5.4	304	2	Q6JHT7_ASF	Q6jht7	african swi
295	95.5	5.4	340	2	Q61349_MOUSE	Q61349	mus musculu
296	95.5	5.4	365	1	CXAR_MOUSE	P97792	mus musculu
297	95.5	5.4	448	2	Q9JHL7_RAT	Q9jhl7	rattus norv
298	95.5	5.4	458	2	Q63093_RAT	Q63093	rattus norv
299	95.5	5.4	459	2	Q9JHL6_RAT	Q9jhl6	rattus norv
300	95.5	5.4	463	2	Q4VAH7_MOUSE	Q4vah7	mus musculu
301	95.5	5.4	463	2	Q66J72_XENLA	Q66j72	xenopus lae
302	95.5	5.4	628	2	Q7S409_NEUCR	Q7s409	neurospora
303	95.5	5.4	700	1	PTPRE_HUMAN	P23469	homo sapien
304	95.5	5.4	700	2	Q5VWH4_HUMAN	Q5vwh4	homo sapien
305	95.5	5.4	771	1	PIGR_MOUSE	070570	mus musculu
306	95.5	5.4	822	1	CAN3_SHEEP	Q9tth8	ovis aries
307	95.5	5.4	1684	2	Q7RIA5_PLAYO	Q7ria5	plasmodium
308	95	5.3	248	2	Q3TQ52_MOUSE	Q3tq52	mus musculu
309	95	5.3	352	2	Q3TV22_MOUSE	Q3tv22	mus musculu
310	95	5.3	577	2	Q2QD17_PONPY	Q2qd17	pongo pygma
311	95	5.3	589	2	Q5REH9_PONPY	Q5reh9	pongo pygma
312	95	5.3	772	2	Q5R770_PONPY	Q5r770	pongo pygma
313	95	5.3	814	2	Q5U495_XENLA	Q5u495	xenopus lae
314	95	5.3	1237	1	PUNC_HUMAN	Q8ivu1	homo sapien
315	95	5.3	228	2	Q610C8_CAEBR	Q610c8	caenorhabdi
316	94.5	5.3	280	2	Q1LWN8_BRARE	Q1lwn8	brachydanio
317	94.5	5.3	280	2	Q8UWK3_ICTPU	Q8uwk3	ictalurus p
318	94.5	5.3	379	2	Q8BLX5_MOUSE	Q8blx5	mus musculu
319	94.5	5.3	397	2	Q8BFX8_MOUSE	Q8bfx8	m adult fem
320	94.5	5.3	404	1	UE1D1_PONPY	Q5r8x4	pongo pygma
321	94.5	5.3	588	2	Q6MG92_RAT	Q6mg92	rattus norv
322	94.5	5.3	840	2	Q3ZVQ3_SPICI	Q3zvq3	spiroplasma

No.	Accession	Species	Name	N	Len	Score	%
324	P23505	rattus norv	GP42_RAT	1	233	5.3	94
325	Q1lwn9	brachydanio	Q1LWN9_BRARE	2	233	5.3	94
326	Q5c8p0	simian aden	Q5C8P0_9ADEN	2	269	5.3	94
327	Q8wnv8	felis silve	Q8WNV8_FELCA	2	328	5.3	94
328	Q178v7	aedes aegyp	Q178V7_AEDAE	2	343	5.3	94
329	Q96q15	homo sapien	Q96Q15_HUMAN	2	419	5.3	94
330	Q32pl9	brachydanio	Q32PL9_BRARE	2	484	5.3	94
331	Q8c8t7	mus musculu	Q8C8T7_MOUSE	2	828	5.3	94
332	Q2h127	chaetomium	Q2H127_CHAGB	2	926	5.3	94
333	P16170	xenopus lae	NCA11_XENLA	1	1088	5.3	94
334	Q9r066	rattus norv	CXAR_RAT	1	365	5.3	93.5
335	Q5m7a4	rattus norv	UE1D1_RAT	1	403	5.3	93.5
336	Q5blw6	bos taurus	Q5BLW6_BOVIN	2	491	5.3	93.5
337	Q4t854	tetraodon n	Q4T854_TETNG	2	572	5.3	93.5
338	Q4vyd6	spiroplasma	Q4VYD6_SPICI	2	840	5.3	93.5
339	Q5t377	homo sapien	Q5T377_HUMAN	2	1039	5.3	93.5
340	Q4rrt1	tetraodon n	Q4RRT1_TETNG	2	1098	5.3	93.5
341	Q2qle0	sus scrofa	MET_PIG	1	1381	5.3	93.5
342	Q1t780	eptatretus	Q1T780_EPTBU	2	126	5.2	93
343	Q6xjv4	mus musculu	Q6XJV4_MOUSE	2	270	5.2	93
344	Q7kr15	drosophila	Q7KR15_DROME	2	339	5.2	93
345	Q91b00	sphoeroides	Q91B00_9PERC	2	342	5.2	93
346	Q384b1	mus musculu	Q384B1_MUSMC	2	397	5.2	93
347	Q00888	homo sapien	PSG4_HUMAN	2	419	5.2	93
348	Q13046	homo sapien	PSG7_HUMAN	2	419	5.2	93
349	Q4by51	crocosphaer	Q4BY51_CROWT	2	455	5.2	93
350	P52200	spiroplasma	PYRG_SPICI	1	535	5.2	93
351	Q5rfw1	mus musculu	Q5RFW1_MOUSE	2	661	5.2	93
352	Q9dgn6	gallus gall	Q9DGN6_CHICK	2	752	5.2	93
353	Q0bqc3	mus musculu	PUNC_MOUSE	2	813	5.2	93
354	Q6fkb0	candida gla	Q6FKB0_CANGA	2	949	5.2	93
355	Q4bi79	burkholderi	Q4BI79_BURVI	2	1028	5.2	93
356	Q3uq28	mus musculu	Q3UQ28_MOUSE	2	1475	5.2	93
357	Q91aj0	xenopus lae	Q91AJ0_XENLA	2	1788	5.2	93
358	Q8c239	m b6-derive	Q8C239_MOUSE	2	160	5.2	92.5
359	Q9y624	homo sapien	JAM1_HUMAN	1	299	5.2	92.5
360	Q6fib4	homo sapien	Q6FIB4_HUMAN	2	299	5.2	92.5
361	P42071	oryctolagus	CD86_RABIT	1	330	5.2	92.5
362	Q5e9j9	bos taurus	Q5E9J9_BOVIN	2	373	5.2	92.5
363	Q5qns6	brachydanio	Q5QNS6_BRARE	2	491	5.2	92.5
364	Q6uxg8	homo sapien	BTNL9_HUMAN	1	535	5.2	92.5
365	Q7zz85	brachydanio	Q7ZZ85_BRARE	2	544	5.2	92.5
366	Q90460	brachydanio	CD166_BRARE	1	564	5.2	92.5
367	Q61qx4	brachydanio	Q61QX4_BRARE	2	564	5.2	92.5
368	Q8ebb5	shewanella	Q8EBB5_SHEON	2	760	5.2	92.5
369	Q9c9s3	arabidopsis	Q9C9S3_ARATH	2	761	5.2	92.5
370	Q7raq7	plasmodium	Q7RAQ7_PLAYO	2	777	5.2	92.5
371	Q8jyb8	porcine lym	Q8JYB8_9GAMA	2	782	5.2	92.5
372	Q8b3u9	porcine lym	Q8B3U9_9GAMA	2	782	5.2	92.5
373	Q28y51	drosophila,	Q28Y51_DROPS	2	1435	5.2	92.5
374	Q5rip6	brachydanio	Q5RIP6_BRARE	2	5533	5.2	92.5
375	Q63476	rattus norv	Q63476_RAT	2	297	5.2	92.5
376	Q68cr6	homo sapien	Q68CR6_HUMAN	2	419	5.2	92
377	Q9uq74	homo sapien	PSG8_HUMAN	2	426	5.2	92
378	Q9ykd7	homo sapien	Q4ZFY1_HUMAN	2	491	5.2	92
379	Q9ykd7	rinderpest	Q9YKD7_9PARA	2	609	5.2	92
380	Q7tsu7	mus musculu	KIRR2_MOUSE	1	700	5.2	92
381	Q3tb04	mus musculu	Q3TB04_MOUSE	2	737	5.2	92
382	Q6p1m7	homo sapien	Q6P1M7_HUMAN	2	743	5.2	92
383	Q715l2	bacillus th	Q715L2_BACTO	2	789	5.2	92
384	Q9zqx3	arabidopsis	Q9ZQX3_ARATH	2	822	5.2	92
385	Q8bie6	mus musculu	FRM4A_MOUSE	1	1020	5.2	92
386	Q7xtp6	oryza sativ	Q7XTP6_ORYSA	2	1025	5.2	92
387	Q7zy71	xenopus lae	Q7ZY71_XENLA	2	1087	5.2	92
388	Q229k4	tetrahymena	Q229K4_TETTH	2	1632	5.2	92
389	Q4srx6	tetraodon n	Q4SRX6_TETTH	2	2008	5.2	92
390	Q9nr99	homo sapien	Q9NR99_HUMAN	2	2828	5.2	92
391	Q1t779	eptatretus	Q1T779_EPTBU	2	121	5.2	91.5
392	Q8c254	mus musculu	Q8C254_MOUSE	2	160	5.2	91.5
393	Q90z86	brachydanio	Q90Z86_BRARE	2	230	5.2	91.5
394	Q7tsa3	mus musculu	BTLA_MOUSE	1	230	5.2	91.5
395	Q4szul	tetraodon n	Q4SZU1_TETNG	2	306	5.2	91.5
396					527	5.2	91.5

Rank	%	Score	Length	Flag	Entry	Organism
397	91.5	5.2	725	2	Q4VWT3_9PIPI	xenopus sp.
398	91.5	5.2	943	2	Q7PRK4_ANOGA	anopheles g
399	91.5	5.2	1079	2	Q9YW56_MSEPV	melanoplus
400	91.5	5.2	1390	1	MET_PANTR	pan troglod
401	91.5	5.2	1390	1	MET_PONPY	pongo pygma
402	91.5	5.2	3005	2	Q50LG3_ALTAL	alternaria
403	91	5.1	308	1	CD276_XENLA	xenopus lae
404	91	5.1	467	2	Q3TZU5_MOUSE	mus musculu
405	91	5.1	467	2	Q91VT9_MOUSE	mus musculu
406	91	5.1	467	2	Q8C6F2_MOUSE	mus musculu
407	91	5.1	491	1	KCNS3_RABIT	oryctolagus
408	91	5.1	510	2	Q9BGY6_MACFA	macaca fasc
409	91	5.1	722	2	Q4KMG2_HUMAN	homo sapien
410	91	5.1	822	1	CAN3_BOVIN	bos taurus
411	91	5.1	1150	2	Q6PCX3_MOUSE	mus musculu
412	91	5.1	1379	2	Q4SMF3_TETNG	tetraodon n
413	91	5.1	1496	2	Q92626_HUMAN	homo sapien
414	91	5.1	1548	1	JAD1D_MOUSE	mus musculu
415	91	5.1	1840	1	CO5A1_RAT	rattus norv
416	91	5.1	2053	1	DSCL1_HUMAN	homo sapien
417	90.5	5.1	230	2	Q801W9_BRARE	brachydanio
418	90.5	5.1	243	2	Q6IAZ2_HUMAN	homo sapien
419	90.5	5.1	306	2	Q32MV8_MOUSE	mus musculu
420	90.5	5.1	325	2	Q5PSW9_PIG	sus scrofa
421	90.5	5.1	331	2	Q22U28_TETTH	tetrahymena
422	90.5	5.1	391	2	Q76CT6_MOUSE	mus musculu
423	90.5	5.1	412	2	Q9R1E1_RAT	rattus norv
424	90.5	5.1	412	2	Q5U334_RAT	rattus norv
425	90.5	5.1	412	2	Q63611_RAT	rattus norv
426	90.5	5.1	417	1	PVR_HUMAN	homo sapien
427	90.5	5.1	474	1	Q5FV48_FUGRU	fugu rubrip
428	90.5	5.1	483	2	Q7SX76_BRARE	brachydanio
429	90.5	5.1	549	2	Q1S5M0_MEDTR	medicago tr
430	90.5	5.1	786	2	Q3EA93_ARATH	arabidopsis
431	90.5	5.1	795	2	Q50NM7_ENTHI	entamoeba h
432	90.5	5.1	795	2	Q1EQ31_ENTHI	entamoeba h
433	90.5	5.1	840	2	Q3ZVP2_SPICI	spiroplasma
434	90.5	5.1	901	2	Q6IR38_MOUSE	mus musculu
435	90.5	5.1	922	2	Q9LTL7_ARATH	arabidopsis
436	90.5	5.1	1012	1	ROBO4_MOUSE	mus musculu
437	90.5	5.1	1041	2	Q1RIT6_RICBR	rickettsia
438	90.5	5.1	1381	2	Q2VHX7_PIG	sus scrofa
439	90.5	5.1	1596	2	Q5CPM9_CRYPV	cryptospori
440	90.5	5.1	1905	1	Y659_PASMU	pasteurella
441	90	5.1	240	2	Q5T325_HUMAN	homo sapien
442	90	5.1	250	1	LFA3_HUMAN	homo sapien
443	90	5.1	250	2	Q5U053_HUMAN	homo sapien
444	90	5.1	309	2	Q91YV7_MOUSE	mus musculu
445	90	5.1	329	2	Q2GX88_CHAGB	chaetomium
446	90	5.1	348	1	NEGR1_MOUSE	mus musculu
447	90	5.1	410	2	Q2SJD1_HAHCH	hahella che
448	90	5.1	419	1	PSG1_HUMAN	homo sapien
449	90	5.1	426	2	Q6ICR4_HUMAN	homo sapien
450	90	5.1	515	2	Q4RP84_TETNG	tetraodon n
451	90	5.1	541	1	IL18R_HUMAN	homo sapien
452	90	5.1	541	2	Q52LC9_HUMAN	homo sapien
453	90	5.1	609	2	Q9WHH7_9PARA	rinderpest
454	90	5.1	625	2	Q2PQQ5_GLOMR	glossina mo
455	90	5.1	742	2	Q3G536_9DELT	pelobacter
456	90	5.1	771	1	Q4KMQ7_HUMAN	homo sapien
457	90	5.1	1179	2	Q7QXR2_GIALA	giardia lam
458	90	5.1	1290	2	Q6WLB5_9DIPT	chaetopsis
459	90	5.1	1297	2	Q4RVK8_TETNG	tetraodon n
460	90	5.1	1431	2	Q80U60_MOUSE	mus musculu
461	90	5.1	10495	2	Q4RE92_TETNG	tetraodon n
462	89.5	5.1	243	1	CD48_HUMAN	homo sapien
463	89.5	5.1	243	2	Q5U055_HUMAN	homo sapien
464	89.5	5.1	266	2	Q2UXN7_DROSI	drosophila
465	89.5	5.1	339	2	Q4T512_TETNG	tetraodon n
466	89.5	5.1	349	1	OMPA_BUCAI	buchnera ap
467	89.5	5.1	358	2	Q1T2T4_MEDTR	medicago tr
468	89.5	5.1	508	2	Q5KU88_GEOKA	geobacillus
469	89.5	5.1	570	2	Q1HGM9_HUMAN	homo sapien

Rank	%	Score	Length	Flag	Entry	Accession	Organism
470	89.5	5.1	570	2	Q5R640_PONPY	Q5r640	pongo pygma
471	89.5	5.1	629	2	Q4DG60_TRYCR	Q4dg60	trypanosoma
472	89.5	5.1	756	2	Q8CJW2_STRCO	Q8cjw2	streptomyce
473	89.5	5.1	770	2	Q89LN9_BRAJA	Q89ln9	bradyrhizob
474	89.5	5.1	794	2	Q2Y2Q9_TOXGO	Q2y2q9	toxoplasma
475	89.5	5.1	821	2	CAN3_PIG	P43368	sus scrofa
476	89.5	5.1	833	2	Q9BPQ7_HALRO	Q9bpq7	halocynthia
477	89.5	5.1	845	2	SLIK2_HUMAN	Q9h156	homo sapien
478	89.5	5.1	845	2	Q2KHN3_HUMAN	Q2khn3	homo sapien
479	89.5	5.1	845	2	Q6AI13_HUMAN	Q6ai13	homo sapien
480	89.5	5.1	917	2	Q36U40_MARHY	Q36u40	marinobacte
481	89.5	5.1	1024	2	FRM4A_HUMAN	Q9p2q2	homo sapien
482	89.5	5.1	1170	2	Q4YR59_PLABE	Q4yr59	plasmodium
483	89.5	5.1	1644	2	Q9W3D2_DROME	Q9w3d2	drosophila
484	89.5	5.1	1671	2	Q9W3D3_DROME	Q9w3d3	drosophila
485	89.5	5.1	1683	2	Q17PQ8_AEDAE	Q17pq8	aedes aegyp
486	89.5	5.1	1716	2	Q61ZV2_CAEBR	Q61zv2	caenorhabdi
487	89.5	5.1	2214	2	SVIL_HUMAN	O95425	homo sapien
488	89.5	5.1	3193	2	Q7RL38_PLAYO	Q7rl38	plasmodium
489	89	5.0	240	1	Q9BRW0_HUMAN	Q9brw0	homo sapien
490	89	5.0	309	1	CD86_MOUSE	P42082	mus musculu
491	89	5.0	309	2	Q549Q9_MOUSE	Q549q9	mus musculu
492	89	5.0	314	2	Q61238_MOUSE	Q61238	mus musculu
493	89	5.0	322	2	Q9PTR8_9PERC	Q9ptr8	sphoeroides
494	89	5.0	323	2	Q8MKZ7_DROME	Q8mkz7	drosophila
495	89	5.0	333	2	Q2EGT7_BRARE	Q2egt7	brachydanio
496	89	5.0	341	2	Q3LFS9_MOUSE	Q3lfs9	mus musculu
497	89	5.0	344	2	Q3S4B2_MUSMC	Q3s4b2	mus musculu
498	89	5.0	356	2	Q64381_MOUSE	Q64381	mus musculu
499	89	5.0	368	2	Q5BI25_DROME	Q5bi25	drosophila
500	89	5.0	434	2	Q6DN72_HUMAN	Q6dn72	homo sapien
501	89	5.0	466	2	Q55IY7_CRYNE	Q55iy7	cryptococcu
502	89	5.0	475	2	Q5C7Z4_SCHJA	Q5c7z4	schistosoma
503	89	5.0	506	2	Q6MG91_RAT	Q6mg91	rattus norv
504	89	5.0	821	2	CAN3_HUMAN	P20807	homo sapien
505	89	5.0	1803	2	Q5CMX4_CRYHO	Q5cmx4	cryptospori
506	89	5.0	5175	2	Q8I0L3_CAEEL	Q8i0l3	caenorhabdi
507	88.5	5.0	5198	2	O76518_CAEEL	O76518	caenorhabdi
508	88.5	5.0	269	2	Q16E78_AEDAE	Q16e78	aedes aegyp
509	88.5	5.0	271	1	OX2V_HHV8	P88963	human herpe
510	88.5	5.0	271	2	O40948_HHV8	O40948	human herpe
511	88.5	5.0	271	2	Q4S7L7_TETNG	Q46717	tetraodon n
512	88.5	5.0	315	2	Q9DGI5_CHICK	Q9dgi5	gallus gall
513	88.5	5.0	316	2	Q5F3J1_CHICK	Q5f3j1	gallus gall
514	88.5	5.0	325	2	Q8UWL3_ICTPU	Q8uwl3	ictalurus p
515	88.5	5.0	327	1	MOX2R_RAT	Q9ea58	rattus norv
516	88.5	5.0	344	2	Q93242_CHICK	Q93242	gallus gall
517	88.5	5.0	391	2	Q1AN90_MOUSE	Q1an90	mus musculu
518	88.5	5.0	403	2	Q3U8X9_MOUSE	Q3u8x9	mus musculu
519	88.5	5.0	403	2	Q3U9E7_MOUSE	Q3u9e7	mus musculu
520	88.5	5.0	463	2	Q481V7_COLP3	Q481v7	colwellia p
521	88.5	5.0	532	2	Q8WWV6_HUMAN	Q8wwv6	homo sapien
522	88.5	5.0	534	2	Q96SA2_HUMAN	Q96sa2	homo sapien
523	88.5	5.0	554	2	Q9W4R3_DROME	Q9w4r3	drosophila
524	88.5	5.0	620	2	Q6IGL3_DROME	Q6igl3	drosophila
525	88.5	5.0	782	2	Q4SI43_TETNG	Q48i43	tetraodon n
526	88.5	5.0	840	2	Q32VN3_SPICI	Q32vn3	spiroplasma
527	88.5	5.0	1081	2	Q8T4N8_PENSE	Q8t4n8	penaeus sem
528	88.5	5.0	1203	2	Q44B63_SOLUS	Q44b63	solibacter
529	88.5	5.0	1283	2	Q7RQP8_PLAYO	Q7rqp8	plasmodium
530	88.5	5.0	1390	1	MET_HUMAN	P08581	homo sapien
531	88.5	5.0	1404	2	Q16JR6_AEDAE	Q16jr6	aedes aegyp
532	88.5	5.0	1769	2	Q4YQU3_PLABE	Q4yqu3	plasmodium
533	88.5	5.0	2267	2	Q237F9_TETTH	Q237f9	tetrahymena
534	88.5	5.0	14609	2	Q21J20_SACD2	Q21j20	saccharopha
535	88	5.0	259	2	Q3LRW0_MOUSE	Q3lrw0	mus musculu
536	88	5.0	265	2	Q32M82_HUMAN	Q32m82	homo sapien
537	88	5.0	309	2	Q3T9F8_MOUSE	Q3t9f8	mus musculu
538	88	5.0	320	2	Q737C6_BACC1	Q737c6	bacillus ce
539	88	5.0	324	2	Q7TMH2_MOUSE	Q7tmh2	mus musculu
540	88	5.0	329	2	Q9TTF2_CANFA	Q9ttf2	canis famil
541	88	5.0	337	2	Q9IA24_9PERC	Q9ia24	sphoeroides
542	88	5.0	339	2	Q9IB09_9PERC	Q9ib09	sphoeroides

No.	%	Score	Length	Copies	Entry Name	Organism
543	88	5.0	343	2	Q8R4Y0_MOUSE	mus musculu
544	88	5.0	363	1	MURG_BORBU	borrelia bu
545	88	5.0	419	2	Q6P520_HUMAN	homo sapien
546	88	5.0	422	2	Q58124_PYRHO	pyrococcus
547	88	5.0	457	2	Q61396_MOUSE	mus musculu
548	88	5.0	508	1	CP6D5_DROME	drosophila
549	88	5.0	509	1	SHPS1_RAT	r tyrosine-
550	88	5.0	530	2	PVRL2_MOUSE	mus musculu
551	88	5.0	530	2	Q80XJ5_MOUSE	mus musculu
552	88	5.0	607	2	Q4LPC1_9BURK	burkholderi
553	88	5.0	607	2	Q1BTG9_9BURK	burkholderi
554	88	5.0	639	2	Q6PA27_XENLA	xenopus lae
555	88	5.0	668	1	PBS2_YEAST	saccharomyc
556	88	5.0	689	2	Q26HI1_9BACT	flavobacter
557	88	5.0	699	1	PTPRE_MOUSE	mus musculu
558	88	5.0	699	2	Q61042_MOUSE	mus musculu
559	88	5.0	719	2	Q3V1H5_MOUSE	mus musculu
560	88	5.0	805	2	Q17LU5_AEDAE	aedes aegyp
561	88	5.0	821	1	CAN3_RAT	rattus norv
562	88	5.0	837	2	Q8G518_BIFLO	bifidobacte
563	88	5.0	901	2	Q17LU6_AEDAE	aedes aegyp
564	88	5.0	986	2	Q8UVR9_FUGRU	fugu rubrip
565	88	5.0	1092	2	NCA12_XENLA	xenopus lae
566	88	5.0	1112	2	Q60JI0_CAEBR	caenorhabdi
567	88	5.0	1303	2	Q174B0_AEDAE	aedes aegyp
568	88	5.0	1333	2	Q14W26_9HERP	ranid herpe
569	88	5.0	1337	2	Q4RKW0_TETNG	tetraodon n
570	88	5.0	1379	2	Q8I3S7_PLAF7	plasmodium
571	88	5.0	1925	1	PLXD1_HUMAN	homo sapien
572	88	5.0	1946	2	Q4S290_TETNG	tetraodon n
573	88	5.0	2802	2	Q53TG8_HUMAN	homo sapien
574	88	5.0	3007	2	Q14215_HUMAN	homo sapien
575	88	5.0	6669	1	NEBU_HUMAN	homo sapien
576	88	5.0	7100	2	Q17HV9_AEDAE	aedes aegyp
577	88	5.0	11696	2	Q5CV09_CRYPV	cryptospori
578	87.5	4.9	265	1	CEAM7_HUMAN	homo sapien
579	87.5	4.9	276	2	Q64861_9ADEN	human adeno
580	87.5	4.9	276	2	Q98822_ADE41	human adeno
581	87.5	4.9	302	2	Q4JX57_CORJK	corynebacte
582	87.5	4.9	325	2	O02838_PIG	sus scrofa
583	87.5	4.9	332	2	Q640U3_XENTR	xenopus tro
584	87.5	4.9	377	2	Q1Q7W2_PSYCK	psychrobact
585	87.5	4.9	403	1	UE1D1_MOUSE	mus musculu
586	87.5	4.9	403	2	Q3TG27_MOUSE	mus musculu
587	87.5	4.9	415	2	Q1L8Z5_BRARE	brachydanio
588	87.5	4.9	416	2	Q56A45_BRARE	brachydanio
589	87.5	4.9	422	1	KI3L1_RAT	rattus norv
590	87.5	4.9	464	2	Q6GL25_XENTR	xenopus tro
591	87.5	4.9	484	2	Q2WEN9_HUMAN	homo sapien
592	87.5	4.9	487	1	FGRL1_CHICK	gallus gall
593	87.5	4.9	547	2	Q6MG93_RAT	rattus norv
594	87.5	4.9	581	2	Q6BN45_DEBHA	debaryomyce
595	87.5	4.9	583	2	CD166_MOUSE	mus musculu
596	87.5	4.9	583	-1	CD166_RAT	rattus norv
597	87.5	4.9	583	2	Q54AJ5_MOUSE	mus musculu
598	87.5	4.9	652	2	Q89703_9VIRU	cassava vei
599	87.5	4.9	695	2	Q28CT9_XENTR	xenopus tro
600	87.5	4.9	699	2	Q61V11_CAEBR	caenorhabdi
601	87.5	4.9	722	2	Q3Q455_9GAMM	shewanella
602	87.5	4.9	723	2	Q5HZF8_XENLA	xenopus lae
603	87.5	4.9	769	2	PIGR_RAT	rattus norv
604	87.5	4.9	1035	2	Q3MEV5_ANAVT	anabaena va
605	87.5	4.9	1087	2	Q9PUF6_CHICK	gallus gall
606	87.5	4.9	2307	2	Q80IV2_9PICO	theiler's-l
607	87.5	4.9	2340	2	Q78DX7_MOUSE	mus musculu
608	87.5	4.9	4162	2	Q98918_CHICK	gallus gall
609	87.5	4.9	4283	2	Q9ERV0_RAT	rattus norv
610	87.5	4.9	18074	1	TITIN_DROME	drosophila
611	87	4.9	156	2	Q5AFG8_CANAL	candida alb
612	87	4.9	225	2	Q5NHZ7_FRATT	francisella
613	87	4.9	229	1	Q9R121_RAT	rattus norv
614	87	4.9	252	2	Q3UYJ4_MOUSE	mus musculu
615	87	4.9	291	1	KO152_MOUSE	mus musculu
616	87	4.9	305	2	Q32MV9_MOUSE	Q32mv9 mus musculu
617	87	4.9	337	2	Q5Z8W6_ORYSA	Q5Z8w6 oryza sativ
618	87	4.9	341	2	Q61153_MOUSE	Q61353 mus musculu
619	87	4.9	344	2	Q568F7_BRARE	Q568f7 brachydanio
620	87	4.9	415	2	Q8C6X8_MOUSE	Q8c6x8 mus musculu
621	87	4.9	457	1	CD4_MOUSE	P06332 mus musculu
622	87	4.9	457	2	Q3TSV7_MOUSE	Q3tsv7 m adult mal
623	87	4.9	464	2	Q3K9F5_PSEPF	Q3k9f5 pseudomonas
624	87	4.9	491	1	KCNS3_HUMAN	Q9bq31 homo sapien
625	87	4.9	491	2	Q8BQZ8_MOUSE	Q8bqz8 m adult mal
626	87	4.9	514	2	Q8BH18_MOUSE	Q8bh18 m 10 days n
627	87	4.9	521	2	CD166_RABIT	O46651 oryctolagus
628	87	4.9	522	2	Q8F7F1_LEPIN	Q8f7f1 leptospira
629	87	4.9	543	2	Q4R603_MACFA	Q4r603 macaca fasc
630	87	4.9	551	2	Q4QQE7_SCHMA	Q4qqe7 schistosoma
631	87	4.9	583	1	CD166_HUMAN	Q13740 homo sapien
632	87	4.9	583	2	Q1HGM8_HUMAN	Q1hgm8 homo sapien
633	87	4.9	609	2	Q7EYK0_ORYSA	Q7eyk0 oryza sativ
634	87	4.9	841	2	Q1RPV5_CIOIN	Q1rpv5 ciona intes
635	87	4.9	946	2	Q2D8C3_ACICY	Q2d8c3 acidiphiliu
636	87	4.9	1149	2	Q2EY14_BRARE	Q2ey14 brachydanio
637	87	4.9	1187	2	Q2U635_ASPOR	Q2u635 aspergillus
638	87	4.9	1272	2	Q4JDD5_BRARE	Q4jdd5 brachydanio
639	87	4.9	1272	2	Q5GIT3_BRARE	Q5git3 brachydanio
640	87	4.9	1284	2	Q5KLV6_CRYNE	Q5klv6 cryptococcu
641	87	4.9	1381	1	MET_HORSE	Q2q1a9 equus cabal
642	87	4.9	1403	2	Q6DCT7_XENLA	Q6dct7 xenopus lae
643	87	4.9	1451	2	Q5SY32_CRYNE	Q5sy32 cryptococcu
644	87	4.9	1497	2	Q5XJV4_MOUSE	Q5xjv4 mus musculu
645	87	4.9	1501	2	Q7TT17_MOUSE	Q7tt17 mus musculu
646	87	4.9	1569	2	Q6PACO_MOUSE	Q6paco mus musculu
647	87	4.9	1666	1	MYOM1_MOUSE	Q62234 mus musculu
648	87	4.9	1666	2	Q546T8_MOUSE	Q546t8 mus musculu
649	87	4.9	1904	2	Q64699_MOUSE	Q64699 mus musculu
650	87	4.9	1907	2	Q4JFC7_MOUSE	Q4jfc7 mus musculu
651	87	4.9	3160	2	FREM2_MOUSE	Q6nvd0 mus musculu
652	87	4.9	3160	2	Q1XGY5_MOUSE	Q1xgy5 mus musculu
653	87	4.9	3707	2	PGBM_MOUSE	Q05793 homo sapien
654	87	4.9	5635	2	HMCNI_HUMAN	Q96rw7 homo sapien
655	86.5	4.9	121	2	Q1T778_EPTBU	Q1t778 eptatretus
656	86.5	4.9	210	2	Q4R7W7_MACFA	Q4r7w7 macaca fasc
657	86.5	4.9	237	2	Q61B65_HUMAN	Q61b65 homo sapien
658	86.5	4.9	240	2	Q6MG96_RAT	Q6mg96 rattus norv
659	86.5	4.9	293	2	Q8AXN8_CYPCA	Q8axn8 cyprinus ca
660	86.5	4.9	299	2	Q2WGK1_CERAE	Q2wgk1 cercopithec
661	86.5	4.9	313	2	O35531_RAT	O35531 rattus norv
662	86.5	4.9	324	2	Q91AY9_9PERC	Q91ay9 9phoeroides
663	86.5	4.9	354	2	NEGR1_PONPY	Q5r412 pongo pygma
664	86.5	4.9	384	2	Q4SY83_TETNG	Q4sy83 tetraodon n
665	86.5	4.9	443	2	EX7L_VIBVU	Q8df05 vibrio vuln
666	86.5	4.9	443	2	EX7L_VIBVY	O7mne3 vibrio vuln
667	86.5	4.9	474	2	P79355_FELCA	P79355 felis silve
668	86.5	4.9	528	2	Q5RTP5_DEIRA	Q5rtp5 deinococcus
669	86.5	4.9	530	2	Q5FVC5_RAT	Q5fvc5 rattus norv
670	86.5	4.9	538	2	Q18JH9_9EURY	Q18jh9 9eury
671	86.5	4.9	626	2	Q4SMS6_TETNG	Q4sms6 tetraodon n
672	86.5	4.9	650	2	Q88BN9_PSESM	Q88bn9 pseudomonas
673	86.5	4.9	683	2	Q2UA88_ASPOR	Q2ua88 aspergillus
674	86.5	4.9	711	2	Q6LJA1_PHOPR	Q6lja1 photobacter
675	86.5	4.9	841	2	Q4DUY0_TRYCR	Q4duy0 trypanosoma
676	86.5	4.9	846	1	SLIK2_MOUSE	Q810co mus musculu
677	86.5	4.9	957	2	Q4E485_TRYCR	Q4e485 trypanosoma
678	86.5	4.9	1028	2	Q6INB5_XENLA	Q6inb5 xenopus lae
679	86.5	4.9	1029	2	Q4Y4R9_PLACH	Q4y4r9 plasmodium
680	86.5	4.9	1381	1	MET_CALJA	Q2qlg5 callithrix
681	86.5	4.9	1390	2	Q21BF2_GORGO	Q21bf2 gorilla gor
682	86.5	4.9	2752	2	Q7QKD0_ANOGA	Q7qkd0 anopheles g
683	86	4.9	235	2	Q4SQ01_TETNG	Q4sq01 tetraodon n
684	86	4.9	259	1	Q9Y5B2_HUMAN	Q9y5b2 homo sapien
685	86	4.9	265	2	Q69R3_9ADEN	Q69r3 simian aden
686	86	4.9	280	2	Q8UWK1_ICTPU	Q8uwk1 ictalurus p
687	86	4.9	339	2	Q91AZ1_9PERC	Q9iaz1 sphoeroides
688	86	4.9	348	1	NEGR1_RAT	Q90oj8 rattus norv

#	Score	%	Length	Identifier	N	Species
689	4.9	86	354	VGLI_VZVD	1	varicella-z
690	4.9	86	354	Q98VN1_HHV3	2	human herpe
691	4.9	86	354	Q77JF6_HHV3	2	human herpe
692	4.9	86	354	Q775H3_VZVE	2	varicella-z
693	4.9	86	354	Q77NN4_HHV3	2	human herpe
694	4.9	86	413	Q6ZNI1_HUMAN	2	homo sapien
695	4.9	86	428	PSG3_HUMAN	1	homo sapien
696	4.9	86	471	Q61KI8_CAEBR	2	caenorhabdi
697	4.9	86	486	Q82NI6_STRAW	2	streptomyce
698	4.9	86	487	Q82MI3_STRAW	2	streptomyce
699	4.9	86	513	Q499T3_RAT	2	rattus norv
700	4.9	86	545	Q9VCT4_DROME	2	drosophila
701	4.9	86	553	Q1SU85_MEDTR	2	medicago tr
702	4.9	86	556	Q58EQ1_BRARE	2	brachydanio
703	4.9	86	648	Q6DJ24_XENTR	2	xenopus tro
704	4.9	86	687	Q9MAJ5_ARATH	2	arabidopsis
705	4.9	86	728	Q762C8_HUMAN	2	homo sapien
706	4.9	86	731	Q8SPI6_MACEU	2	macropus eu
707	4.9	86	864	Q228C6_TETTH	2	tetrahymena
708	4.9	86	885	RFL1_ARATH	1	arabidopsis
709	4.9	86	1036	Q2T5R6_BURTA	2	burkholderi
710	4.9	86	1070	Q4S2F2_TETNG	2	tetraodon n
711	4.9	86	1150	Q2VWP7_HUMAN	2	homo sapien
712	4.9	86	1187	Q98TF0_CYPCA	2	cyprinus ca
713	4.9	86	1252	Q6CUN8_KLULA	2	kluyveromyc
714	4.9	86	1437	O15070_HUMAN	2	homo sapien
715	4.9	86	1667	Q465V8_METBF	2	methanosarc
716	4.9	86	22017	Q7ZZ46_BRARE	2	brachydanio
717	4.8	85.5	230	Q5SNP6_BRARE	2	brachydanio
718	4.8	85.5	235	Q6GMW6_HUMAN	2	homo sapien
719	4.8	85.5	249	Q6XJV6_MOUSE	2	mus musculu
720	4.8	85.5	269	Q3TDV9_MOUSE	2	mus musculu
721	4.8	85.5	278	Q3U4D2_MOUSE	2	mus musculu
722	4.8	85.5	315	Q2IFG0_ANADE	2	anaeromyxob
723	4.8	85.5	324	Q9UPK9_HUMAN	2	homo sapien
724	4.8	85.5	326	Q9UPK8_HUMAN	2	homo sapien
725	4.8	85.5	332	Q4RFH3_TETNG	2	tetraodon n
726	4.8	85.5	333	O75238_HUMAN	2	homo sapien
727	4.8	85.5	335	O75237_HUMAN	2	homo sapien
728	4.8	85.5	347	Q4R908_MACFA	2	macaca fasc
729	4.8	85.5	393	Q7TNZ6_RAT	2	rattus norv
730	4.8	85.5	412	Q1W649_ICTPU	2	ictalurus p
731	4.8	85.5	412	Q1W650_ICTPU	2	ictalurus p
732	4.8	85.5	487	Q3UL03_MOUSE	2	mus musculu
733	4.8	85.5	488	Q5FYV4_SPHEL	2	sphingomona
734	4.8	85.5	510	Q5US57_XENLA	2	xenopus lae
735	4.8	85.5	527	Q6YW20_ORYSA	2	oryza sativ
736	4.8	85.5	604	Q2ZJR0_CALSA	2	caldicellul
737	4.8	85.5	620	Q4S1C0_TETNG	2	tetraodon n
738	4.8	85.5	622	Q50XJ4_ENTHI	2	entamoeba h
739	4.8	85.5	650	Q8NA84_HUMAN	2	homo sapien
740	4.8	85.5	657	Q93D79_BACTU	2	bacillus th
741	4.8	85.5	689	Q47Q15_THEFY	2	thermobifid
742	4.8	85.5	723	Q3NLU7_SHEFR	2	shewanella
743	4.8	85.5	767	Q5LBX5_BACFN	2	bacteroides
744	4.8	85.5	767	Q64SV4_BACFR	2	bacteroides
745	4.8	85.5	788	Q5JZZ0_BACTU	2	bacillus th
746	4.8	85.5	789	Q938Z1_BACTU	2	bacillus th
747	4.8	85.5	789	Q4VYT0_BACTU	2	bacillus th
748	4.8	85.5	789	O69270_BACTU	2	bacillus th
749	4.8	85.5	789	Q45793_BACTU	2	bacillus th
750	4.8	85.5	789	Q5XPQ5_BACTU	2	bacillus th
751	4.8	85.5	789	Q58I33_BACTU	2	bacillus th
752	4.8	85.5	789	Q58XI2_BACTU	2	bacillus th
753	4.8	85.5	789	Q45792_BACTU	2	bacillus th
754	4.8	85.5	789	Q3ZKK4_BACTU	2	bacillus th
755	4.8	85.5	789	Q79SG2_BACTU	2	bacillus th
756	4.8	85.5	789	Q19UY6_BACTA	2	bacillus th
757	4.8	85.5	925	Q17RK4_HUMAN	2	homo sapien
758	4.8	85.5	978	KFMS_FSVMD	1	feline sarc
759	4.8	85.5	1048	Q337L8_ORYSA	2	oryza sativ
760	4.8	85.5	1101	Q9FWL8_ORYSA	2	oryza sativ
761	4.8	85.5				

#	Score	%	Length	Identifier	N	Accession / Species
762	4.8	85.5	1354	Q9VIC7_DROME	2	Q9vic7 drosophila
763	4.8	85.5	1363	Q53P57_ORYSA	2	Q53p57 oryza sativ
764	4.8	85.5	1416	Q4P2B6_USTMA	2	Q4p2b6 ustilago ma
765	4.8	85.5	1587	Q7Q5D1_ANOGA	2	Q7q5d1 anopheles g
766	4.8	85.5	1808	Q24B12_TETTH	2	Q24b12 tetrahymena
767	4.8	85.5	1947	Q7RQQ4_PLAYO	2	Q7rqq4 plasmodium
768	4.8	85.5	2096	Q466C0_METBF	2	Q466c0 methanosarc
769	4.8	85.5	2115	Q8IE55_PLAF7	2	Q8ie55 plasmodium
770	4.8	85.5	2129	Q6FUN0_CANGA	2	Q6fun0 candida gla
771	4.8	85.5	2225	Q54C68_DICDI	2	Q54c68 dictyosteli
772	4.8	85.5	2414	Q59EZ3_HUMAN	2	Q59ez3 homo sapien
773	4.8	85.5	2491	MPRI_HUMAN	1	P11717 h cation-in
774	4.8	85.5	2588	NSD1_MOUSE	1	O88491 mus musculu
775	4.8	85.5	2623	Q6WRI0_HUMAN	2	Q6wri0 homo sapien
776	4.8	85.5	4379	Q3ART7_CHLCH	2	Q3art7 chlorobium
777	4.8	85.5	4662	Q17317_AEDAE	2	Q17317 aedes aegyp
778	4.8	85	224	Q870G0_PODAN	2	Q870g0 podospora a
779	4.8	85	280	Q8UWL1_ICTPU	2	Q8uwl1 ictalurus p
780	4.8	85	293	Q6MG56_RAT	2	Q6mg56 rattus norv
781	4.8	85	332	Q8EXS1_LEPIN	2	Q8exs1 leptospira
782	4.8	85	332	Q75FS2_LEPIC	2	Q75fs2 leptospira
783	4.8	85	375	Q93GD6_DESAF	2	Q93gd6 desulfovibr
784	4.8	85	379	JAML1_MOUSE	1	Q80u19 mus musculu
785	4.8	85	402	RAGE_RAT	1	Q63495 rattus norv
786	4.8	85	402	Q6MG86_RAT	2	Q6mg86 rattus norv
787	4.8	85	409	Q2ATV6_9BACI	2	Q2atv6 bacillus we
788	4.8	85	475	Q6NZH8_XENTR	2	Q6nzh8 xenopus tro
789	4.8	85	480	Q1QTF6_CHRSD	2	Q1qtf6 chromohalob
790	4.8	85	570	Q6GLY1_XENLA	2	Q6gly1 xenopus lae
791	4.8	85	583	CD166_BOVIN	1	Q9bh13 bos taurus
792	4.8	85	684	Q21138_CAEEL	2	Q21138 caenorhabdi
793	4.8	85	709	Q9XSJ2_PIG	2	Q9xsj2 sus scrofa
794	4.8	85	712	Q59EB3_HUMAN	2	Q59eb3 homo sapien
795	4.8	85	821	CAN3_MOUSE	1	Q64691 mus musculu
796	4.8	85	875	Q91ZY7_MOUSE	2	Q91zy7 mus musculu
797	4.8	85	880	Q6A7L8_PROAC	2	Q6a718 propionibac
798	4.8	85	883	Q23BA7_TETTH	2	Q23ba7 tetrahymena
799	4.8	85	969	Q248S7_TETTH	2	Q248s7 tetrahymena
800	4.8	85	976	Q58N28_9CAUD	2	Q58n28 cyanophage
801	4.8	85	977	Q3U3W0_MOUSE	2	Q3u3w0 mus musculu
802	4.8	85	1168	Q4UEU6_THEAN	2	Q4ueu6 theileria a
803	4.8	85	1184	Q23NH5_TETTH	2	Q23nh5 tetrahymena
804	4.8	85	1376	Q8AZ23_9GAMA	2	Q8az23 porcine lym
805	4.8	85	1384	Q76915_BOVIN	2	Q76915 bos taurus
806	4.8	85	1389	Q4VA61_MOUSE	2	Q4va61 mus musculu
807	4.8	85	1723	Q8CHB2_MOUSE	2	Q8chb2 mus musculu
808	4.8	85	2170	SDK2_HUMAN	1	Q58ex2 homo sapien
809	4.8	85	2487	Q9N1T0_ORNAN	2	Q9n1t0 ornithorhyn
810	4.8	84.5	160	Q171N6_AEDAE	2	Q171n6 aedes aegyp
811	4.8	84.5	210	Q7PVM1_ANOGA	2	Q7pvm1 anopheles g
812	4.8	84.5	238	Q749M2_GEOSL	2	Q749m2 geobacter s
813	4.8	84.5	241	Q4T4Z6_TETNG	2	Q4t4z6 tetraodon n
814	4.8	84.5	263	Q4SQQ2_TETNG	2	Q4sqq2 tetraodon n
815	4.8	84.5	280	Q899D0_CLOTE	2	Q899d0 clostridium
816	4.8	84.5	289	Q5HZV8_XENTR	2	Q5hzv8 xenopus tro
817	4.8	84.5	292	KO152_HUMAN	1	Q14165 homo sapien
818	4.8	84.5	303	PILRA_HUMAN	1	Q9ukj1 homo sapien
819	4.8	84.5	308	Q4YCN2_PLABE	2	Q4ycn2 plasmodium
820	4.8	84.5	337	CLM1_MOUSE	1	Q68jq7 mus musculu
821	4.8	84.5	344	Q22FK2_TETTH	2	Q22fk2 tetrahymena
822	4.8	84.5	354	NEGR1_HUMAN	1	Q7z3b1 homo sapien
823	4.8	84.5	394	Q9D0G8_MOUSE	2	Q9d0g8 mus musculu
824	4.8	84.5	397	Q6XRC3_HUMAN	2	Q6xrc3 homo sapien
825	4.8	84.5	431	Q3UUJ4_MOUSE	2	Q3uuj4 mus musculu
826	4.8	84.5	533	Q4IDN9_GIBZE	2	Q4idn9 gibberella
827	4.8	84.5	551	Q466F5_METBF	2	Q466f5 methanosarc
828	4.8	84.5	605	Q4UG78_THEAN	2	Q4ug78 theileria a
829	4.8	84.5	656	O04533_ARATH	2	O04533 arabidopsis
830	4.8	84.5	759	Q369A6_9GAMM	2	Q369a6 shewanella
831	4.8	84.5	779	Q4CX14_TRYCR	2	Q4cx14 trypanosoma
832	4.8	84.5	798	Q86K66_DICDI	2	Q86k66 dictyosteli
833	4.8	84.5	798	Q54ZZ6_DICDI	2	Q54zz6 dictyosteli
834	4.8	84.5	840	Q7VQI2_BLOFL	2	Q7vqi2 blochmannia

No.	Score	%	Accession	Entry	N	Length	Organism
835	4.8	84.5	Q8px58	Q8PX58_METMA	2	1164	methanosarc
836	4.8	84.5	M10l1	M10L1_HUMAN	1	1211	homo sapien
837	4.8	84.5	Q4rh47	Q4RH47_TETNG	2	1485	tetraodon n
838	4.8	84.5	Q8pvi0	Q8PVI0_METMA	2	1608	methanosarc
839	4.8	84.5	Q4dnh6	Q4DNH6_TRYCR	2	3441	trypanosoma
840	4.8	84.5	Q7yqk5	Q7YQK5_CANFA	2	4311	canis famil
841	4.7	84	Q5vsn2	Q5VSN2_BRARE	2	237	brachydanio
842	4.7	84	Q9ptr7	Q9PTR7_9PERC	2	262	sphoeroides
843	4.7	84	Q9ib04	Q9IB04_9PERC	2	333	sphoeroides
844	4.7	84	Q8bys4	Q8BYS4_MOUSE	2	343	mus musculu
845	4.7	84	Q4dz01	Q4DZ01_TRYCR	2	361	trypanosoma
846	4.7	84	Murg_borga	MURG_BORGA	1	363	borrelia ga
847	4.7	84	Q5v6f5	Q5V6F5_HALMA	2	381	haloarcula
848	4.7	84	Q21iz0	Q21IZ0_SACD2	2	403	saccharopha
849	4.7	84	Q8enx5	Q8ENX5_OCEIH	2	403	oceanobacil
850	4.7	84	Q501t5	Q501T5_BRARE	2	418	brachydanio
851	4.7	84	Q5kcr5	Q5KCR5_CRYNE	2	453	cryptococcu
852	4.7	84	Q6fag8	Q6FAG8_ACIAD	2	457	acinetobact
853	4.7	84	Q4kfa6	Q4KFA6_PSEF5	2	464	pseudomonas
854	4.7	84	Q5kcr4	Q5KCR4_CRYNE	2	466	cryptococcu
855	4.7	84	Q6p6i8	Q6P6I8_MOUSE	2	509	mus musculu
856	4.7	84	Q7zzu8	Q7ZZU8_BRARE	2	556	brachydanio
857	4.7	84	Q2frc9	Q2FRC9_METHJ	2	566	methanospir
858	4.7	84	Q8nkb1	Q8NKB1_EMENI	2	593	emericella
859	4.7	84	Q5l8s3	Q5L8S3_BACFN	2	594	bacteroides
860	4.7	84	Q238p3	Q238P3_TETTH	2	609	tetrahymena
861	4.7	84	Q5zdk0	Q5ZDK0_ORYSA	2	611	oryza sativ
862	4.7	84	Q73tm4	Q73TM4_MYCPA	2	611	mycobacteri
863	4.7	84	Q54hg9	Q54HG9_DICDI	2	685	dictyosteli
864	4.7	84	Q1vxy2	Q1VXY2_9FLAO	2	709	psychroflex
865	4.7	84	Q3v3b0	Q3V3B0_MOUSE	2	727	mus musculu
866	4.7	84	O97754	O97754_RABIT	2	775	oryctolagus
867	4.7	84	Q2fqf7	Q2FQF7_METHJ	2	787	methanospir
868	4.7	84	Q8h329	Q8H329_ORYSA	2	800	oryza sativ
869	4.7	84	Q8t3j2	Q8T3J2_DROME	2	810	drosophila
870	4.7	84	Q9vk54	Q9VK54_DROME	2	811	drosophila
871	4.7	84	Q8mz57	Q8M257_DROME	2	812	drosophila
872	4.7	84	Q9ux76	Q9UX76_SULSO	2	851	sulfolobus
873	4.7	84	Q2xy30	Q2XY30_DROSI	2	864	drosophila
874	4.7	84	Q2xy31	Q2XY31_DROSI	2	864	drosophila
875	4.7	84	Q2xy32	Q2XY32_DROME	2	864	drosophila
876	4.7	84	Q2xy27	Q2XY27_DROER	2	867	drosophila
877	4.7	84	Q4cys5	Q4CYS5_TRYCR	2	872	trypanosoma
878	4.7	84	P91643	P91643_DROME	2	880	drosophila
879	4.7	84	Q4imf4	Q4IMF4_GIBZE	2	984	gibberella
880	4.7	84	Q7xtp5	Q7XTP5_ORYSA	2	1028	oryza sativ
881	4.7	84	Q997a4	Q997A4_9BROM	2	1062	american pl
882	4.7	84	Q6fxs8	Q6FXS8_CANGA	2	1098	candida gla
883	4.7	84	Q5um15	Q5UM15_BRARE	2	1115	brachydanio
884	4.7	84	Q17n93	Q17N93_AEDAE	2	1126	aedes aegyp
885	4.7	84	Q17n94	Q17N94_AEDAE	2	1155	aedes aegyp
886	4.7	84	Q9vqw1	Q9VQW1_DROME	2	1193	drosophila
887	4.7	84	Q4ih28	Q4IH28_GIBZE	2	1206	gibberella
888	4.7	84	Insrr_mouse	INSRR_MOUSE	1	1300	mus musculu
889	4.7	84	Met_mouse	MET_MOUSE	1	1379	mus musculu
890	4.7	84	Q90815	Q90815_CHICK	2	1499	gallus gall
891	4.7	84	Q571l9	Q571L9_MOUSE	2	1671	mus musculu
892	4.7	84	Q5spj6	Q5SPJ6_MOUSE	2	1903	mus musculu
893	4.7	84	Q4cs58	Q4CS58_TRYCR	2	2292	trypanosoma
894	4.7	84	Celr1_mouse	CELR1_MOUSE	1	3034	mus musculu
895	4.7	83.5	Q2bx11	Q2BX11_9GAMM	2	210	photobacter
896	4.7	83.5	Q2xyv9	Q2XYV9_VARDU	2	241	varanus dum
897	4.7	83.5	Q23hx8	Q23HX8_TETTH	2	247	tetrahymena
898	4.7	83.5	Q3lrv9	Q3LRV9_MOUSE	2	263	mus musculu
899	4.7	83.5	Q4swl7	Q4SWL7_TETNG	2	270	tetraodon n
900	4.7	83.5	Q9gl33	Q9GL33_BOVIN	2	284	bos taurus
901	4.7	83.5	Q8k3j3	Q8K3J3_MERUN	2	289	meriones un
902	4.7	83.5	Q3kpi0	Q3KPI0_HUMAN	2	293	homo sapien
903	4.7	83.5	Jam2_human	JAM2_HUMAN	1	298	homo sapien
904	4.7	83.5	Q6pyw4	Q6PYW4_SCHJA	2	306	schistosoma
905	4.7	83.5	Q50082	Q50082_PYRHO	2	315	pyrococcus
906	4.7	83.5	Q2aqa6	Q2AQA6_9BACI	2	391	bacillus we
907	4.7	83.5	Q6f5f0	Q6F5F0_MOUSE	2	391	mus musculu
908	4.7	83.5	O76708	O76708_CAEEL	2	392	caenorhabdi
909	4.7	83.5	Q91wp1	Q91WP1_MOUSE	2	408	mus musculu
910	4.7	83.5	Q8bvf6	Q8BVF6_MOUSE	2	408	mus musculu
911	4.7	83.5	Q8k094	Q8K094_MOUSE	2	408	m polioviru
912	4.7	83.5	Q1fsz9	Q1FSZ9_9CHLR	2	432	roseiflexus
913	4.7	83.5	Q6uxi0	Q6UXI0_HUMAN	2	450	homo sapien
914	4.7	83.5	Q96pj5	Q96PJ5_HUMAN	2	515	homo sapien
915	4.7	83.5	Q96re0	Q96RE0_HUMAN	2	515	homo sapien
916	4.7	83.5	P91670	P91670_DROME	2	528	drosophila
917	4.7	83.5	Q81h34	Q81H34_BACCR	2	577	bacillus ce
918	4.7	83.5	Q6c7f7	Q6C7F7_YARLI	2	580	yarrowia li
919	4.7	83.5	Q3ewn8	Q3EWN8_BACTI	2	597	borrelia th
920	4.7	83.5	Q899y4	Q899Y4_CLOTE	2	646	clostridium
921	4.7	83.5	Q2x5y6	Q2X5Y6_9GAMM	2	719	shewanella
922	4.7	83.5	Q2zs23	Q2ZS23_SHEPU	2	719	shewanella
923	4.7	83.5	Q512d5	Q512D5_CANFA	2	725	canis famil
924	4.7	83.5	Q4yb64	Q4YB64_PLABE	2	738	plasmodium
925	4.7	83.5	Q3iet5	Q3IET5_PSBHT	2	820	pseudoalter
926	4.7	83.5	Q512d7	Q512D7_CANFA	2	847	canis famil
927	4.7	83.5	Q4sap3	Q4SAP3_TETNG	2	862	tetraodon n
928	4.7	83.5	Q2sea0	Q2SEA0_HAHCH	2	870	hahella che
929	4.7	83.5	Q5r6d4	Q5R6D4_PONPY	2	1028	pongo pygma
930	4.7	83.5	Q9de49	Q9DE49_BRARE	2	1059	brachydanio
931	4.7	83.5	Q5t2b6	Q5T2B6_BRARE	2	1101	brachydanio
932	4.7	83.5	Q6g587	Q6G587_BARHE	2	1160	bartonella
933	4.7	83.5	Q4t5j1	Q4T5J1_TETNG	2	1273	tetraodon n
934	4.7	83.5	Q6frx7	Q6FRX7_CANGA	2	1332	candida gla
935	4.7	83.5	Q22qv2	Q22QV2_TETTH	2	1386	tetrahymena
936	4.7	83.5	Q22sp9	Q22SP9_TETTH	2	1462	tetrahymena
937	4.7	83.5	O55124	O55124_MOUSE	2	1463	mus musculu
938	4.7	83.5	Q5cyr5	Q5CYR5_CRYPV	2	1483	cryptospori
939	4.7	83.5	Q4jfl8	Q4JFL8_RAT	2	1501	rattus norv
940	4.7	83.5	Q9qw00	Q9QW00_9MURI	2	1501	rattus sp.
941	4.7	83.5	Q83nf7	Q83NF7_TROW8	2	1556	tropheryma
942	4.7	83.5	Q9j5c2	Q9J5C2_FOWPV	2	1802	fowlpox vir
943	4.7	83.5	Q64605	Q64605_RAT	2	1863	rattus norv
944	4.7	83.5	Q3kre9	Q3KRE9_RAT	2	1907	rattus norv
945	4.7	83.5	Q16pl9	Q16PL9_AEDAE	2	3652	aedes aegyp
946	4.7	83.5	Q7pl01	Q7PL01_ANOGA	2	4658	anopheles g
947	4.7	83	Q7y889	Q7Y889_PIG	2	151	sus scrofa
948	4.7	83	Q8wyy6	Q8WYY6_HUMAN	2	231	homo sapien
949	4.7	83	Q78t27	Q78T27_MOUSE	2	234	mus musculu
950	4.7	83	Q1j854	Q1J854_STRPF	2	235	streptococc
951	4.7	83	Q6dqx5	Q6DQX5_RABIT	2	237	oryctolagus
952	4.7	83	Q5vyi6	Q5VYI6_HUMAN	2	273	homo sapien
953	4.7	83	Q8cje8	Q8CJE8_MESAU	2	281	mesocricetu
954	4.7	83	Q62s95	Q62S95_HUMAN	2	305	homo sapien
955	4.7	83	Q3tdr5	Q3TDR5_MOUSE	2	309	mus musculu
956	4.7	83	Q91az2	Q91AZ2_9PERC	2	339	sphoeroides
957	4.7	83	Q16m91	Q16M91_AEDAE	2	348	aedes aegyp
958	4.7	83	Q93ew5	Q93EW5_DESDE	2	369	desulfovibr
959	4.7	83	Q8tu74	Q8TU74_METAC	2	373	methanosarc
960	4.7	83	O08835	O08835_CERAE	2	401	cercopithec
961	4.7	83	Q68dm9	Q68DM9_HUMAN	2	420	homo sapien
962	4.7	83	Q6clk2	Q6CLK2_KLULA	2	424	kluyveromyc
963	4.7	83	Q90wi4	Q90WI4_CHICK	2	437	gallus gall
964	4.7	83	Q4rkf5	Q4RKF5_TETNG	2	438	tetraodon n
965	4.7	83	Q6lu33	Q6LU33_PHOPR	2	448	photobacter
966	4.7	83	O05139	STHA_PSEFL	1	463	pseudomonas
967	4.7	83	Q9h0c3	Q9HOC3_HUMAN	2	514	homo sapien
968	4.7	83	Q465j1	Q465J1_METBF	2	530	methanosarc
969	4.7	83	Q9dfu0	Q9DFU0_SPAAU	2	538	sparus aura
970	4.7	83	Q50z57	Q50Z57_ENTHI	2	545	entamoeba h
971	4.7	83	Q59hd7	Q59HD7_HUMAN	2	555	homo sapien
972	4.7	83	Q9d2z1	Q9D2Z1_MOUSE	2	577	mus musculu
973	4.7	83	Q2aup8	Q2AUP8_9BACI	2	580	bacillus we
974	4.7	83	Q64ny2	Q64NY2_BACFR	2	594	bacteroides
975	4.7	83	Q4s767	Q4S767_TETNG	2	702	tetraodon n
976	4.7	83	Q23jz6	Q23JZ6_TETTH	2	717	tetrahymena
977	4.7	83	P81265	PIGR_BOVIN	1	757	bos taurus
978	4.7	83	Q387s6	Q387S6_9TRYP	2	812	trypanosoma
979	4.7	83	Q5vvf5	Q5VVF5_HUMAN	2	845	homo sapien
980	4.7	83	Q2xy28	Q2XY28_DROYA	2	871	drosophila

Index	Length	Cnt	Score	%	Accession	Code	Organism
981	871	2	4.7	83	Q2XY29_DROYA	Q2xy29	drosophila
982	873	1	4.7	83	VLDLR_HUMAN	P98155	homo sapien
983	873	2	4.7	83	Q6S4M1_MACMU	Q6s4m1	macaca mula
984	922	2	4.7	83	Q3U4N8_MOUSE	Q3u4n8	mus musculu
985	925	2	4.7	83	Q9UB95_CAEEL	Q9ub95	caenorhabdi
986	925	2	4.7	83	Q9U4E4_CAEEL	Q9u4e4	caenorhabdi
987	925	2	4.7	83	O44191_CAEEL	O44191	caenorhabdi
988	925	2	4.7	83	Q9UB94_CAEEL	Q9ub94	caenorhabdi
989	1099	2	4.7	83	Q61KC1_CAEBR	Q61kc1	caenorhabdi
990	1106	2	4.7	83	ACLY_CAEEL	P53585	caenorhabdi
991	1106	2	4.7	83	Q8IBR5_PLAF7	Q8ibr5	plasmodium
992	1254	2	4.7	83	Q674V1_PODCA	Q674v1	podocoryne
993	1382	2	4.7	83	Q64GK4_BRARE	Q64gk4	brachydanio
994	1419	2	4.7	83	Q4RWP2_TETNG	Q4rwp2	tetraodon n
995	1639	2	4.7	83	Q3Y5G6_TRICA	Q3y5g6	tribolium c
996	1657	2	4.7	83	Q2J5B0_FRASC	Q2j5b0	frankia sp.
997	1919	2	4.7	83	Q1T6Y3_APIME	Q1t6y3	apis mellif
998	2421	2	4.7	83	Q95MJ1_LEMCA	Q95mj1	lemur catta
999	2489	1	4.7	83	Q06116_YEAST	Q06116	saccharomyc
1000	3862	2	4.7	83	Q2SAM3_HAHCH	Q2sam3	hahella che
1001	3976	2	4.7	83	Q2SKC0_HAHCH	Q2skc0	hahella che
1002	140	2	4.7	82.5	Q5VWH6_HUMAN	Q5vwh6	homo sapien
1003	154	2	4.7	82.5	Q5VWH5_HUMAN	Q5vwh5	homo sapien
1004	155	2	4.7	82.5	Q96P81_HUMAN	Q96p81	homo sapien
1005	218	2	4.7	82.5	Q4JLL4_LACRE	Q4jll4	lactobacill
1006	230	2	4.7	82.5	Q8UV76_BRARE	Q8uv76	brachydanio
1007	239	2	4.7	82.5	Q61BJ5_CAEBR	Q61bj5	caenorhabdi
1008	244	2	4.7	82.5	Q7YS40_PIG	Q7ys40	sus scrofa
1009	288	2	4.7	82.5	Q4D3U2_TRYCR	Q4d3u2	trypanosoma
1010	319	1	4.7	82.5	GPA33_MOUSE	Q9jka5	mus musculu
1011	330	2	4.7	82.5	P97269_CAVPO	P97269	cavia porce
1012	332	1	4.7	82.5	CLM1_RAT	Q566e6	rattus norv
1013	336	2	4.7	82.5	Q33VZ2_9GAMM	Q33vz2	shewanella
1014	341	2	4.7	82.5	BTNL1_MOUSE	Q7tst0	mus musculu
1015	363	2	4.7	82.5	Q31XA4_SHIBS	Q31xa4	shigella bo
1016	364	2	4.7	82.5	Q4KK51_PSEF5	Q4kk51	pseudomonas
1017	370	2	4.7	82.5	Q3AB46_CARHZ	Q3ab46	carboxydoth
1018	377	2	4.7	82.5	Q4R920_MACFA	Q4r920	macaca fasc
1019	378	1	4.7	82.5	LPAT4_ARATH	Q8l4y2	arabidopsis
1020	382	2	4.7	82.5	Q6VEU7_MOUSE	Q6veu7	mus musculu
1021	409	2	4.7	82.5	Q1HTU9_9POXV	Q1htu9	squirrelpox
1022	437	2	4.7	82.5	Q5LZV9_STRT1	Q5lzv9	streptococc
1023	437	2	4.7	82.5	Q5M4H0_STRT2	Q5m4h0	streptococc
1024	446	2	4.7	82.5	Q8NK03_EMENI	Q8nk03	emericella
1025	446	2	4.7	82.5	Q5B2Q4_EMENI	Q5b2q4	emericella
1026	468	1	4.7	82.5	Q6PJ50_MOUSE	Q6pj50	mus musculu
1027	488	2	4.7	82.5	Q3VW96_PROAE	Q3vw96	prosthecoch
1028	540	2	4.7	82.5	Q582F7_9TRYP	Q582f7	trypanosoma
1029	540	2	4.7	82.5	Q8TQK0_METAC	Q8tqk0	methanosarc
1030	580	2	4.7	82.5	Q30Q08_THIDN	Q30q08	thiomicrosp
1031	616	2	4.7	82.5	Q1DXQ5_COCIM	Q1dxq5	coccidioide
1032	623	2	4.7	82.5	Q4D8Q4_TRYCR	Q4d8q4	trypanosoma
1033	653	2	4.7	82.5	Q3BYU3_XANC5	Q3byu3	xanthomonas
1034	676	2	4.7	82.5	Q4SIF9_TETNG	Q4sif9	tetraodon n
1035	703	2	4.7	82.5	Q23RG9_TETTH	Q23rg9	tetrahymena
1036	773	1	4.7	82.5	MES2_CAEEL	O17514	caenorhabdi
1037	789	2	4.7	82.5	Q4U3F5_BACTU	Q4u3f5	bacillus th
1038	833	2	4.7	82.5	Q9VHG1_DROME	Q9vhg1	drosophila
1039	840	2	4.7	82.5	Q84BZ6_SPIKU	Q84bz6	spiroplasma
1040	840	2	4.7	82.5	Q84BZ7_SPIKU	Q84bz7	spiroplasma
1041	986	2	4.7	82.5	Q6DG17_BRARE	Q6dg17	brachydanio
1042	994	2	4.7	82.5	Q61OQ4_CAEBR	Q61oq4	caenorhabdi
1043	994	2	4.7	82.5	Q96167_PLAF7	Q96167	plasmodium
1044	1025	2	4.7	82.5	Q2C478_9GAMM	Q2c478	photobacter
1045	1028	1	4.7	81.5	CNTN6_HUMAN	Q9ug52	homo sapien
1046	1028	2	4.7	81.5	Q2KHM2_HUMAN	Q2khm2	homo sapien
1047	1209	2	4.7	81.5	Q7PG72_ANOGA	Q7pg72	anopheles g
1048	1215	2	4.7	81.5	Q7QEC1_ANOGA	Q7qec1	anopheles g
1049	1241	2	4.7	81.5	Q83GQ1_TROWT	Q83gq1	tropheryma
1050	1345	2	4.7	81.5	Q9BJF3_OXYTR	Q9bjf3	oxytricha t
1051	1381	2	4.7	81.5	Q2IBC0_RHIFE	Q2ibc0	rhinolophus
1052	1397	2	4.7	81.5	Q4PEN2_USTMA	Q4pen2	ustilago ma
1053	1457	2	4.7	81.5	Q1L8D7_BRARE	Q1l8d7	brachydanio

Index	Length	Cnt	Score	%	Accession	Code	Organism
1054	1501	2	4.7	82.5	Q2M3R7_HUMAN	Q2m3r7	homo sapien
1055	1560	2	4.7	82.5	Q59FX6_HUMAN	Q59fx6	homo sapien
1056	1567	2	4.7	82.5	Q6MIA1_BDEBA	Q6mia1	bdellovibri
1057	1642	2	4.7	82.5	Q515F7_ENTHI	Q515f7	entamoeba h
1058	2597	2	4.7	82.5	Q6WRH9_RAT	Q6wrh9	rattus norv
1059	4034	2	4.7	82.5	Q6ZX14_MAGGR	Q6zx14	magnaporthe
1060	4256	2	4.7	82.5	Q8MJF3_CANFA	Q8mjf3	canis famil
1061	34350	1	4.7	82.5	TITIN_HUMAN	Q8wz42	homo sapien
1062	151	2	4.6	82	Q7YS88_PIG	Q7ys88	sus scrofa
1063	184	2	4.6	82	Q7VM71_HAEDU	Q7vm71	haemophilus
1064	214	2	4.6	82	Q4SX01_TETNG	Q4sx01	tetraodon n
1065	219	2	4.6	82	Q41PA4_METBU	Q41pa4	methanococc
1066	276	2	4.6	82	Q28G33_XENTR	Q28g33	xenopus tro
1067	308	2	4.6	82	Q95K99_MACFA	Q95k99	macaca fasc
1068	324	2	4.6	82	Q8NBY8_HUMAN	Q8nby8	homo sapien
1069	326	2	4.6	82	Q8NC17_HUMAN	Q8nc17	homo sapien
1070	327	1	4.6	82	VSIG2_HUMAN	Q96iq7	homo sapien
1071	331	2	4.6	82	Q9IB01_9PERC	Q9ib01	sphoeroides
1072	361	2	4.6	82	Q1SI62_MEDTR	Q1si62	medicago tr
1073	376	2	4.6	82	Q482D4_COLP3	Q482d4	colwellia p
1074	380	2	4.6	82	Q2YHU2_CHICK	Q2yhu2	gallus gall
1075	383	2	4.6	82	Q5RJS5_RAT	Q5rjs5	rattus norv
1076	386	1	4.6	82	NATB_BACSU	P46904	bacillus su
1077	386	2	4.6	82	Q5BZ00_SCHJA	Q5bz00	schistosoma
1078	395	2	4.6	82	Q4SLB1_TETNG	Q4slb1	tetraodon n
1079	409	2	4.6	82	Q814M1_BACCR	Q814m1	bacillus ce
1080	412	2	4.6	82	Q8HY14_RABIT	Q8hy14	oryctolagus
1081	444	2	4.6	82	Q8S917_ARATH	Q8s917	arabidopsis
1082	449	2	4.6	82	P78721_ORPSP	P78721	orpinomyces
1083	508	2	4.6	82	Q4SJF6_TETNG	Q4sjf6	tetraodon n
1084	509	2	4.6	82	Q61YK3_CAEBR	Q61yk3	caenorhabdi
1085	554	2	4.6	82	Q5BAI9_EMENI	Q5bai9	emericella
1086	585	2	4.6	82	Q43M41_SOLUS	Q43m41	solibacter
1087	587	2	4.6	82	Q9IAA1_CARAU	Q9iaa1	carassius a
1088	609	1	4.6	82	HEMA_RINDR	P41355	rinderpest
1089	609	1	4.6	82	Q6LAC4_9PARA	Q6lac4	rinderpest
1090	636	2	4.6	82	Q5LHT2_BACFN	Q5lht2	bacteroides
1091	636	2	4.6	82	Q64YT4_BACFR	Q64yt4	bacteroides
1092	637	1	4.6	82	PLB1_CRYNE	Q9p8l1	cryptococcu
1093	709	2	4.6	82	Q9XSJ1_BOVIN	Q9xsj1	bos taurus
1094	709	2	4.6	82	O08702_RAT	O08702	rattus norv
1095	737	2	4.6	82	O70376_RAT	O70376	rattus norv
1096	745	2	4.6	82	Q59UZ6_CANAL	Q59uz6	candida alb
1097	757	2	4.6	82	O70482_RAT	O70482	rattus norv
1098	785	2	4.6	82	Q9QZF9_RAT	Q9qzf9	rattus norv
1099	880	1	4.6	82	TYRO3_MOUSE	P55144	mus musculu
1100	880	2	4.6	82	Q6NZM6_MOUSE	Q6nzm6	mus musculu
1101	912	2	4.6	82	Q4KKU8_HUMAN	Q4kku8	homo sapien
1102	977	2	4.6	82	Q3U210_MOUSE	Q3u210	mus musculu
1103	1007	1	4.6	82	GRID2_HUMAN	O43424	homo sapien
1104	1007	2	4.6	82	Q4KKU5_HUMAN	Q4kku5	homo sapien
1105	1009	2	4.6	82	Q4KKV0_HUMAN	Q4kkv0	homo sapien
1106	1038	2	4.6	82	Q59FZ1_HUMAN	Q59fz1	homo sapien
1107	1166	2	4.6	82	Q8CHA3_MOUSE	Q8cha3	mus musculu
1108	1358	2	4.6	82	Q80VP0_MOUSE	Q80vp0	mus musculu
1109	1803	2	4.6	82	Q6PA47_XENLA	Q6pa47	xenopus lae
1110	2036	2	4.6	82	Q5CRN8_CRYPV	Q5crn8	cryptospori
1111	2262	2	4.6	82	GRIPE_HUMAN	Q6gyq0	homo sapien
1112	2289	2	4.6	82	Q5CID4_CRYHO	Q5cid4	cryptospori
1113	2940	2	4.6	82	Q4S3T6_TETNG	Q4s3t6	tetraodon n
1114	3173	1	4.6	82	Q8IHP9_PLAF7	Q8ihp9	plasmodium
1115	3562	2	4.6	82	Q882M6_PSESM	Q882m6	pseudomonas
1116	178	2	4.6	81.5	CSPG2_CHICK	Q90953	gallus gall
1117	206	2	4.6	81.5	Q1DGQ9_AEDAE	Q1dgq9	aedes aegyp
1118	211	2	4.6	81.5	Q6MY89_ASPFU	Q6my89	aspergillus
1119	236	2	4.6	81.5	Q7PVK5_ANOGA	Q7pvk5	anopheles g
1120	265	2	4.6	81.5	Q6P5S3_HUMAN	Q6p5s3	homo sapien
1121	265	2	4.6	81.5	Q2D4X3_9FIRM	Q2d4x3	desulfotoma
1122	278	2	4.6	81.5	Q8AVV1_XENLA	Q8avv1	xenopus lae
1123	278	1	4.6	81.5	OX2G_RAT	P04218	rattus norv
1124	301	2	4.6	81.5	Q7Q864_ANOGA	Q7q864	anopheles g
1125	302	1	4.6	81.5	ICOSL_HUMAN	O75144	homo sapien
1126	329	2	4.6	81.5	Q9IAY6_9PERC	Q9iay6	sphoeroides

Index	Length	N	81.5	4.6	ID_CODE	Organism
1127	336	2	81.5	4.6	Q90ZB9_BRARE	brachydanio
1128	340	2	81.5	4.6	Q91AZ6_9PERC	sphoeroides
1129	352	2	81.5	4.6	Q08266_HUMAN	homo sapien
1130	352	2	81.5	4.6	Q15403_HUMAN	homo sapien
1131	355	1	81.5	4.6	XCP1_ARATH	arabidopsis
1132	373	1	81.5	4.6	Q66HD4_RAT	rattus norv
1133	378	1	81.5	4.6	LEUK_RAT	rattus norv
1134	390	2	81.5	4.6	Q55IR6_CRYNE	cryptococcu
1135	402	2	81.5	4.6	Q62G94_ORYSA	oryza sativ
1136	411	2	81.5	4.6	Q15228_HUMAN	homo sapien
1137	427	2	81.5	4.6	Q4N2I2_THEPA	theileria p
1138	438	2	81.5	4.6	Q7T0Z8_XENLA	xenopus lae
1139	440	2	81.5	4.6	Q62MD4_HUMAN	homo sapien
1140	441	2	81.5	4.6	Q17LZ3_AEDAE	aedes aegyp
1141	444	2	81.5	4.6	Q6K2Y8_ORYSA	oryza sativ
1142	473	2	81.5	4.6	Q82QD1_SALTY	salmonella
1143	473	2	81.5	4.6	Q57R32_SALCH	salmonella
1144	474	2	81.5	4.6	Q4HV02_GIBZE	gibberella
1145	478	2	81.5	4.6	Q4UIZ5_THEAN	theileria a
1146	479	2	81.5	4.6	Q6GNX2_XENLA	xenopus lae
1147	490	2	81.5	4.6	Q35SV5_9GAMM	shewanella
1148	493	2	81.5	4.6	Q6CGB7_YARLI	yarrowia li
1149	497	2	81.5	4.6	Q97EZ4_CLOAB	clostridium
1150	502	2	81.5	4.6	Q842D1_ECOLI	escherichia
1151	504	1	81.5	4.6	FGRL1_HUMAN	homo sapien
1152	507	2	81.5	4.6	Q751G2_ASHGO	ashbya goss
1153	521	2	81.5	4.6	Q4CCC5_CLOTM	clostridium
1154	522	2	81.5	4.6	Q64DK4_9ARCH	uncultured
1155	524	2	81.5	4.6	Q75SW4_ECOLI	escherichia
1156	524	2	81.5	4.6	Q09012_SHISO	shigella so
1157	524	2	81.5	4.6	Q3Z2U8_SHISS	shigella so
1158	525	2	81.5	4.6	Q6VMU4_ECOLI	escherichia
1159	525	2	81.5	4.6	Q6VMU6_ECOLI	escherichia
1160	525	2	81.5	4.6	Q6VMU5_ECOLI	escherichia
1161	536	2	81.5	4.6	Q4V5E0_DROME	drosophila
1162	577	2	81.5	4.6	Q23TR7_TETTH	tetrahymena
1163	606	2	81.5	4.6	Q9VMN6_DROME	drosophila
1164	610	2	81.5	4.6	Q4H2Y0_CIOIN	ciona intes
1165	647	2	81.5	4.6	Q50317_BRARE	brachydanio
1166	677	2	81.5	4.6	Q8A3Q5_BACTN	bacteroides
1167	685	2	81.5	4.6	Q2TAE7_XENLA	xenopus lae
1168	708	2	81.5	4.6	Q9M1P4_ARATH	arabidopsis
1169	709	1	81.5	4.6	Y939_SULTO	sulfolobus
1170	719	2	81.5	4.6	Q22700_9GAMM	shewanella
1171	727	2	81.5	4.6	Q5W5X8_XENLA	xenopus lae
1172	746	2	81.5	4.6	Q6DIR2_XENTR	xenopus tro
1173	759	2	81.5	4.6	Q2Z3Q9_9GAMM	shewanella
1174	779	2	81.5	4.6	Q8AAG1_BACTN	bacteroides
1175	797	2	81.5	4.6	Q17CL8_AEDAE	aedes aegyp
1176	806	2	81.5	4.6	Q4S9K9_TETNG	tetraodon n
1177	815	1	81.5	4.6	CAN3_MACFA	macaca fasc
1178	824	2	81.5	4.6	Q8A3C4_BACTN	bacteroides
1179	829	2	81.5	4.6	Q5LGP6_BACFN	bacteroides
1180	833	2	81.5	4.6	Q5RHY1_BRARE	brachydanio
1181	854	2	81.5	4.6	Q61E29_CAEBR	caenorhabdi
1182	857	2	81.5	4.6	Q512D6_CANFA	canis famil
1183	873	2	81.5	4.6	Q42595_XENLA	xenopus lae
1184	873	1	81.5	4.6	CORO7_HUMAN	homo sapien
1185	925	2	81.5	4.6	Q59E18_DROME	drosophila
1186	944	2	81.5	4.6	Q3UKK2_MOUSE	mus musculu
1187	947	2	81.5	4.6	Q54YD8_DICDI	dictyosteli
1188	1005	2	81.5	4.6	Q4YNU8_PLABE	plasmodium
1189	1015	2	81.5	4.6	Q1Z3Q0_PHOPR	photobacter
1190	1050	2	81.5	4.6	Q3Y272_ENTFC	enterococcu
1191	1075	2	81.5	4.6	Q93284_FUGRU	fugu rubrip
1192	1187	2	81.5	4.6	Q93962_9FUNG	glomus vers
1193	1194	2	81.5	4.6	Q7TPV3_MOUSE	mus musculu
1194	1214	2	81.5	4.6	O75054_HUMAN	homo sapien
1195	1214	2	81.5	4.6	Q6ZQA6_MOUSE	mus musculu
1196	1253	2	81.5	4.6	Q4SCT8_TETNG	tetraodon n
1197	1304	2	81.5	4.6	Q5HA85_EHRRW	ehrlichia r
1198	1470	2	81.5	4.6	Q5L5Q3_CHLAB	chlamydophi
1199	1518	2	81.5	4.6	Q5B7W8_EMENI	emericella

Index	81.5	4.6	Length	N	ID_CODE	Accession	Organism
1200	81.5	4.6	1522	2	Q499E3_MOUSE	Q499e3	mus musculu
1201	81.5	4.6	1596	2	Q9HCL6_HUMAN	Q9hcl6	homo sapien
1202	81.5	4.6	1896	2	Q2NFA5_METST	Q2nfa5	methanospha
1203	81.5	4.6	2212	2	Q8NHN3_HUMAN	Q8nhn3	homo sapien
1204	81.5	4.6	2242	2	Q1N5O5_9GAMM	Q1n5o5	oceanobacte
1205	81.5	4.6	2284	2	Q8I5Y7_PLAF7	Q8i5y7	plasmodium
1206	81.5	4.6	7968	1	OBSCN_HUMAN	Q5vst9	homo sapien
1207	81	4.6	149	2	Q86L22_DICDI	Q86122	dictyosteli
1208	81	4.6	149	2	Q55OJ7_DICDI	Q550j7	dictyosteli
1209	81	4.6	151	2	Q867B8_PIG	Q867b8	sus scrofa
1210	81	4.6	233	2	Q4AEV1_9CHLB	Q4aev1	chlorobium
1211	81	4.6	234	2	Q1RMN8_BOVIN	Q1rmn8	bos taurus
1212	81	4.6	241	2	Q2XYW1_HELSU	Q2xyw1	heloderma s
1213	81	4.6	252	2	O95781_HUMAN	O95781	homo sapien
1214	81	4.6	258	2	Q28Y34_DROPS	Q28y34	drosophila
1215	81	4.6	266	2	Q6AYP8_RAT	Q6ayp8	rattus norv
1216	81	4.6	272	2	Q86IJ5_HORSE	Q86ij5	equus cabal
1217	81	4.6	318	2	Q9U3I9_CABEL	Q9u3i9	caenorhabdi
1218	81	4.6	326	2	Q9IAY7_9PERC	Q9iay7	sphoeroides
1219	81	4.6	330	2	Q87W83_PSESM	Q87w83	pseudomonas
1220	81	4.6	333	2	Q5SNP5_BRARE	Q5snp5	brachydanio
1221	81	4.6	338	1	LSAMP_HUMAN	Q13449	homo sapien
1222	81	4.6	350	2	Q2BZ85_9GAMM	Q2bz85	photobacter
1223	81	4.6	352	2	Q2AGE5_9FIRM	Q2age5	halothermot
1224	81	4.6	374	2	Q43741_BROFI	Q43741	bromheadia
1225	81	4.6	378	2	Q4CJM9_CLOTM	Q4cjm9	clostridium
1226	81	4.6	423	2	Q9UAG6_DICDI	Q9uag6	dictyosteli
1227	81	4.6	423	2	Q54D73_DICDI	Q54d73	dictyosteli
1228	81	4.6	425	2	Q61FM2_CAEBR	Q61fm2	caenorhabdi
1229	81	4.6	451	2	Q8DDA0_VIBVU	Q8dda0	vibrio vuln
1230	81	4.6	481	2	Q5K374_BRARE	Q5k374	brachydanio
1231	81	4.6	489	1	CP302_DROME	Cp302	drosophila
1232	81	4.6	491	2	Q1AP76_PIG	Q1ap76	sus scrofa
1233	81	4.6	510	2	Q1HAY8_FUGRU	Q1hay8	fugu rubrip
1234	81	4.6	517	2	Q4RFQ2_TETNG	Q4rfq2	tetraodon n
1235	81	4.6	518	2	Q22D53_TETTH	Q22d53	tetrahymena
1236	81	4.6	521	1	CD166_CANFA	CD166	canis famil
1237	81	4.6	580	2	Q54D58_DICDI	Q54d58	dictyosteli
1238	81	4.6	617	2	Q5MY54_BRARE	Q5my54	brachydanio
1239	81	4.6	624	2	Q94AX9_ARATH	Q94ax9	arabidopsis
1240	81	4.6	630	2	Q1SB03_MEDTR	Q1sb03	medicago tr
1241	81	4.6	643	2	O7Y231_ARATH	O7y231	arabidopsis
1242	81	4.6	648	2	Q6NTL5_XENLA	Q6ntl5	xenopus lae
1243	81	4.6	656	2	Q35A50_9BRAD	Q35a50	bradyrhizob
1244	81	4.6	700	2	Q4O3A0_LEIMA	Q4o3a0	leishmania
1245	81	4.6	745	2	Q6NNX7_DROME	Q6nnx7	drosophila
1246	81	4.6	760	1	YCE5_YEAST	P25574	saccharomyc
1247	81	4.6	769	2	Q97IS9_CLOAB	Q97is9	clostridium
1248	81	4.6	786	2	Q23C84_TETTH	Q23c84	tetrahymena
1249	81	4.6	829	1	CADH3_HUMAN	P22223	homo sapien
1250	81	4.6	917	2	Q4D632_TRYCR	Q4d632	trypanosoma
1251	81	4.6	937	2	Q8G4P3_BIFLO	Q8g4p3	bifidobacte
1252	81	4.6	945	2	Q3U1X4_MOUSE	Q3u1x4	mus musculu
1253	81	4.6	977	2	Q3U1Y3_MOUSE	Q3u1y3	mus musculu
1254	81	4.6	1040	2	Q5RDT8_PONPY	Q5rdt8	pongo pygma
1255	81	4.6	1079	2	Q6E7G6_CANFA	Q6e7g6	canis famil
1256	81	4.6	1102	2	Q3H857_TRIER	Q3h857	trichodesmi
1257	81	4.6	1150	2	Q4SL82_TETNG	Q4sl82	tetraodon n
1258	81	4.6	1180	2	Q5IS40_PANTR	Q5is40	pan troglod
1259	81	4.6	1196	2	Q98TF1_CYPCA	Q98tf1	cyprinus ca
1260	81	4.6	1220	2	Q9P3A8_SCHPO	Q9p3a8	schizosacch
1261	81	4.6	1256	1	ERBB2_MOUSE	P70424	mus musculu
1262	81	4.6	1304	1	NRCAM_HUMAN	Q92823	homo sapien
1263	81	4.6	1335	2	Q51EY2_ENTHI	Q51ey2	entamoeba h
1264	81	4.6	1478	2	Q59H90_HUMAN	Q59h90	homo sapien
1265	81	4.6	1898	2	Q64604_RAT	Q64604	rattus norv
1266	81	4.6	1901	2	Q7UI70_RHOBA	Q7ui70	rhodopirell
1267	81	4.6	2219	2	Q88WI9_LACPL	Q88wi9	lactobacill
1268	81	4.6	2383	2	Q4N957_THEPA	Q4n957	theileria p
1269	81	4.6	2402	2	Q9AER7_STAEP	Q9aer7	staphylococ
1270	81	4.6	2447	2	Q9HKF4_STAEQ	Q9hkf4	staphylococ
1271	81	4.6	2747	2	Q5GQW9_9CAUD	Q5gqw9	bacteriopha
1272	81	4.6	2895	2	Q16GK5_AEDAE	Q16gk5	aedes aegyp

#	Score	PI	Length	Count	Identifier	Accession	Organism
1273	80.5	4.5	128	2	Q3SYF5_HUMAN	Q3SYF5	homo sapien
1274	80.5	4.5	172	2	Q1VYF3_9FLAO	Q1VYF3	psychroflex
1275	80.5	4.5	251	2	Q1LXF9_BRARE	Q1LXF9	brachydanio
1276	80.5	4.5	290	2	Q8CRR9_STAES	Q8CRR9	staphylococ
1277	80.5	4.5	291	2	Q41M17_METBU	Q41M17	methanococc
1278	80.5	4.5	291	2	Q5HN00_STAEQ	Q5HN00	staphylococ
1279	80.5	4.5	291	2	Q22JY8_CALSA	Q22JY8	caldicellul
1280	80.5	4.5	346	1	EFNB1_HUMAN	P98172	homo sapien
1281	80.5	4.5	371	2	Q4MVP1_BACCE	Q4MVP1	bacillus ce
1282	80.5	4.5	371	2	Q3EU96_BACTI	Q3EU96	bacillus th
1283	80.5	4.5	371	2	Q633A8_BACCZ	Q633A8	bacillus ce
1284	80.5	4.5	371	2	Q6HCJ8_BACHK	Q6HCJ8	bacillus th
1285	80.5	4.5	371	2	Q816Y2_BACCR	Q816Y2	bacillus ce
1286	80.5	4.5	371	2	Q72Z49_BACC1	Q72Z49	bacillus ce
1287	80.5	4.5	376	1	GCP1_ARATH	Q94B08	arabidopsis
1288	80.5	4.5	377	2	Q3TCK7_MOUSE	Q3TCK7	mus musculu
1289	80.5	4.5	382	2	Q5XI43_RAT	Q5XI43	rattus norv
1290	80.5	4.5	385	2	Q4SQV8_TETNG	Q4SQV8	tetraodon n
1291	80.5	4.5	388	2	Q8R464_MOUSE	Q8R464	mus musculu
1292	80.5	4.5	388	2	Q1WIM1_RAT	Q1WIM1	rattus norv
1293	80.5	4.5	402	2	Q2GVQ4_CHAGB	Q2GVQ4	chaetomium
1294	80.5	4.5	462	1	MURD_CLOAB	Q97EB9	clostridium
1295	80.5	4.5	472	2	Q811T8_MOUSE	Q811T8	mus musculu
1296	80.5	4.5	473	2	Q5PGH5_SALPA	Q5PGH5	salmonella
1297	80.5	4.5	473	2	Q8Z809_SALTI	Q8Z809	salmonella
1298	80.5	4.5	475	2	Q62056_MOUSE	Q62056	mus musculu
1299	80.5	4.5	476	1	YCAM_ECOLI	P75835	escherichia
1300	80.5	4.5	498	2	Q88BD9_PSESM	Q88BD9	pseudomonas
1301	80.5	4.5	507	2	Q5K4Q3_PIG	Q5K4Q3	sus scrofa
1302	80.5	4.5	514	2	Q5SQU8_MOUSE	Q5SQU8	mus musculu
1303	80.5	4.5	540	2	Q8XEB5_ECO57	Q8XEB5	escherichia
1304	80.5	4.5	546	2	Q80X70_MOUSE	Q80X70	mus musculu
1305	80.5	4.5	548	2	Q99NB3_MOUSE	Q99NB3	mus musculu
1306	80.5	4.5	556	2	Q8DEW4_VIBVU	Q8DEW4	vibrio vuln
1307	80.5	4.5	564	2	Q7ZU00_BRARE	Q7ZU00	brachydanio
1308	80.5	4.5	589	2	Q4CM86_TRYCR	Q4CM86	trypanosoma
1309	80.5	4.5	602	2	Q86YJ9_HUMAN	Q86YJ9	homo sapien
1310	80.5	4.5	634	2	Q1KUW2_9ROSI	Q1KUW2	cleome spin
1311	80.5	4.5	636	2	Q4FWE0_LEIMA	Q4FWE0	leishmania
1312	80.5	4.5	662	2	Q5CRD8_CRYPV	Q5CRD8	cryptospori
1313	80.5	4.5	683	2	Q7XNT7_ORYSA	Q7XNT7	oryza sativ
1314	80.5	4.5	707	2	Q36AK3_9GAMM	Q36AK3	shewanella
1315	80.5	4.5	719	2	Q53FL7_HUMAN	Q53FL7	homo sapien
1316	80.5	4.5	739	2	Q865F2_RABIT	Q865F2	oryctolagus
1317	80.5	4.5	739	2	Q35W63_9GAMM	Q35W63	shewanella
1318	80.5	4.5	759	2	Q7PUU6_ANOGA	Q7PUU6	anopheles g
1319	80.5	4.5	769	2	Q8RSZ5_BACTU	Q8RSZ5	bacillus th
1320	80.5	4.5	789	2	Q44QK6_CHLLI	Q44QK6	chlorobium
1321	80.5	4.5	803	2	Q16WM8_AEDAE	Q16WM8	aedes aegyp
1322	80.5	4.5	814	2	Q39594_CHLRE	Q39594	chlamydomon
1323	80.5	4.5	823	2	Q7TQ14_RAT	Q7TQ14	rattus norv
1324	80.5	4.5	932	2	Q8JFR5_BRARE	Q8JFR5	brachydanio
1325	80.5	4.5	976	2	Q9W755_BRARE	Q9W755	brachydanio
1326	80.5	4.5	976	2	Q5RID5_BRARE	Q5RID5	brachydanio
1327	80.5	4.5	976	2	Q2TXA8_ASPOR	Q2TXA8	aspergillus
1328	80.5	4.5	1006	2	Q2TGG1_CHLTR	Q2TGG1	chlamydia t
1329	80.5	4.5	1032	2	Q4DR51_TRYCR	Q4DR51	trypanosoma
1330	80.5	4.5	1044	2	Q4DYD0_TRYCR	Q4DYD0	trypanosoma
1331	80.5	4.5	1046	2	Q5QG93_MOUSE	Q5QG93	mus musculu
1332	80.5	4.5	1079	2	Q5QGS4_MOUSE	Q5QGS4	mus musculu
1333	80.5	4.5	1114	2	Q6WLA9_9DIPT	Q6WLA9	heterostomu
1334	80.5	4.5	1293	2	Q5A2D6_CANAL	Q5A2D6	candida alb
1335	80.5	4.5	1304	2	BLM_XENLA	Q9DEY9	xenopus lae
1336	80.5	4.5	1364	1	Q5F475_CHICK	Q5F475	gallus gall
1337	80.5	4.5	1389	2	Q3UQS9_MOUSE	Q3UQS9	mus musculu
1338	80.5	4.5	1463	2	Q7Z3Y2_HUMAN	Q7Z3Y2	homo sapien
1339	80.5	4.5	1465	2	Q6UAQ6_CTEID	Q6UAQ6	ctenopharyn
1340	80.5	4.5	1677	2	Q4RJ21_TETNG	Q4RJ21	tetraodon n
1341	80.5	4.5	1702	2	PTPRS_HUMAN	Q13332	homo sapien
1342	80.5	4.5	1948	1	Q22RR6_TETTH	Q22RR6	tetrahymena
1343	80.5	4.5	2146	2	Q5CGS0_CRYHO	Q5CGS0	cryptospori
1344	80.5	4.5	2170	2	Q5CQ17_CRYPV	Q5CQ17	cryptospori
1345	80.5	4.5	2253	2	Q8JV20_9PICO	Q8JV20	ljungan vir
1346	80.5	4.5	2253	2	Q8JV20_9PICO	Q8JV20	ljungan vir
1347	80.5	4.5	2358	2	Q95MJ2_MACRG	Q95MJ2	macropus ru
1348	80.5	4.5	2898	2	Q872P1_NEUCR	Q872P1	neurospora
1349	80.5	4.5	2906	2	Q299Y6_DROPS	Q299Y6	drosophila
1350	80.5	4.5	3267	2	Q5DUA4_MOUSE	Q5DUA4	mus musculu
1351	80.5	4.5	3283	2	Q5DUA5_MOUSE	Q5DUA5	mus musculu
1352	80.5	4.5	3337	2	Q9TWY4_CAEEL	Q9TWY4	caenorhabdi
1353	80.5	4.5	3343	1	CAD3_CAEEL	P34616	caenorhabdi
1354	80.5	4.5	3352	2	Q5DUA3_MOUSE	Q5DUA3	mus musculu
1355	80.5	4.5	3354	1	CAD23_MOUSE	Q99PF4	mus musculu
1356	80.5	4.5	3357	1	CSPG2_MOUSE	Q62059	mus musculu
1357	80.5	4.5	8081	1	UNC89_CAEEL	O01761	caenorhabdi
1358	80.5	4.5	8871	2	Q3ASL6_CHLCH	Q3ASL6	chlorobium
1359	80	4.5	184	2	Q8WVI8_HUMAN	Q8WVI8	homo sapien
1360	80	4.5	227	1	PILRB_HUMAN	Q9UKJ0	homo sapien
1361	80	4.5	235	2	Q99M11_MOUSE	Q99M11	mus musculu
1362	80	4.5	240	2	Q5VSN6_BRARE	Q5VSN6	brachydanio
1363	80	4.5	259	2	Q4CNK7_TRYCR	Q4CNK7	trypanosoma
1364	80	4.5	262	2	Q308M3_HUMAN	Q308M3	homo sapien
1365	80	4.5	276	2	Q640S5_XENTR	Q640S5	xenopus tro
1366	80	4.5	327	2	Q4RTM7_TETNG	Q4RTM7	tetraodon n
1367	80	4.5	337	2	Q8UV29_BRARE	Q8UV29	brachydanio
1368	80	4.5	338	1	LSAMP_RAT	Q62813	rattus norv
1369	80	4.5	338	2	Q3TYE5_MOUSE	Q3TYE5	mus musculu
1370	80	4.5	341	1	KI2L3_HUMAN	P43628	h killer ce
1371	80	4.5	341	1	LSAMP_MOUSE	Q8BLK3	mus musculu
1372	80	4.5	343	2	Q8X5J1_ECO57	Q8X5J1	escherichia
1373	80	4.5	361	2	Q5M960_RAT	Q5M960	rattus norv
1374	80	4.5	365	2	Q8AXL6_ONCMY	Q8AXL6	oncorhynchu
1375	80	-4.5	378	2	Q66MN4_PETMA	Q66MN4	petromyzon
1376	80	4.5	436	2	Q99563_HUMAN	Q99563	homo sapien
1377	80	4.5	436	2	Q4NAS0_9MICC	Q4NAS0	arthrobacte
1378	80	4.5	440	2	Q8MK36_MACMU	Q8MK36	macaca mula
1379	80	4.5	447	2	Q303G5_STRSU	Q303G5	streptococc
1380	80	4.5	465	2	Q67TE8_SYMTH	Q67TE8	symbiobacte
1381	80	4.5	482	1	ARCD_PSEAE	P18275	pseudomonas
1382	80	4.5	492	2	Q6UEG2_ASPPA	Q6UEG2	aspergillus
1383	80	4.5	509	2	Q5CUK7_CRYPV	Q5CUK7	cryptospori
1384	80	4.5	516	2	Q81WX2_HUMAN	Q81WX2	homo sapien
1385	80	4.5	523	2	Q480W4_COLP3	Q480W4	colwellia p
1386	80	4.5	529	1	FGRL1_MOUSE	Q91V87	mus musculu
1387	80	4.5	535	2	Q65J12_BACLD	Q65J12	bacillus li
1388	80	4.5	562	2	Q1KUS7_9ROSI	Q1KUS7	cleome spin
1389	80	4.5	574	2	PVRL3_BRARE	Q58EG3	brachydanio
1390	80	4.5	609	2	Q629I1_RINDK	Q629I1	rinderpest
1391	80	4.5	624	2	Q8LG08_ARATH	Q8LG08	arabidopsis
1392	80	4.5	627	1	PYRG_DROME	Q9VULL	drosophila
1393	80	4.5	633	2	Q7SXC1_BRARE	Q7SXC1	brachydanio
1394	80	4.5	637	1	PLB1_CRYNV	Q9P8P2	cryptococcu
1395	80	4.5	681	2	Q75JX7_DICDI	Q75JX7	dictyosteli
1396	80	4.5	681	2	Q559P6_DICDI	Q559P6	dictyosteli
1397	80	4.5	696	2	Q17IR1_AEDAE	Q17IR1	aedes aegyp
1398	80	4.5	753	2	Q54K07_DICDI	Q54K07	dictyosteli
1399	80	4.5	815	2	Q54VZ8_DICDI	Q54VZ8	dictyosteli
1400	80	4.5	865	2	Q68DA2_HUMAN	Q68DA2	homo sapien
1401	80	4.5	877	2	Q29KN4_DROPS	Q29KN4	drosophila
1402	80	4.5	902	2	BRCC4_CRIGR	Q9QYM7	cricetulus
1403	80	4.5	918	2	Q24IJ9_TETTH	Q24IJ9	tetrahymena
1404	80	4.5	957	2	Q641F3_XENLA	Q641F3	xenopus lae
1405	80	4.5	960	2	Q6BXD5_DEBHA	Q6BXD5	debaryomyce
1406	80	4.5	1000	2	Q4TBR4_TETNG	Q4TBR4	tetraodon n
1407	80	4.5	1005	2	P79921_XENLA	P79921	xenopus lae
1408	80	4.5	1040	1	CNTN2_HUMAN	Q02246	homo sapien
1409	80	4.5	1040	2	Q5T054_HUMAN	Q5T054	homo sapien
1410	80	4.5	1072	2	Q2M080_DROPS	Q2M080	drosophila
1411	80	4.5	1168	2	Q22UQ4_TETTH	Q22UQ4	tetrahymena
1412	80	4.5	1170	1	TSP1_MOUSE	P35441	mus musculu
1413	80	4.5	1170	2	Q3TR40_MOUSE	Q3TR40	mus musculu
1414	80	4.5	1192	2	Q81YZ8_BACAN	Q81YZ8	bacillus an
1415	80	4.5	1207	2	Q3DAM6_STRAG	Q3DAM6	streptococc
1416	80	4.5	1214	2	Q23DY4_TETTH	Q23DY4	tetrahymena
1417	80	4.5	1310	2	Q8I7I4_CAEEL	Q8I7I4	caenorhabdi
1418	80	4.5	1431	2	Q8EW23_MYCPE	Q8EW23	mycoplasma

Left column:

1419	80	4.5	Q9YRB3_9VIRU	Q9yrb3 nudaurelia
1420	80	4.5	Q723M7_LISMF	Q723m7 listeria mo
1421	80	4.5	Q8ITI5_CAEEL	Q8iti5 caenorhabdi
1422	80	4.5	Q22F24_TETTH	Q22f24 tetrahymena
1423	80	4.5	Q4CTN6_TRYCR	Q4ctn6 trypanosoma
1424	80	4.5	Q6UDW7_PLAFA	Q6udw7 plasmodium
1425	80	4.5	Q7RTF4_PLAYO	Q7rtf4 plasmodium
1426	79.5	4.5	Q3TD98_MOUSE	Q3td98 mus musculu
1427	79.5	4.5	Q8C2T1_MOUSE	Q8c2t1 mus musculu
1428	79.5	4.5	Q6PIQ7_HUMAN	Q6piq7 homo sapien
1429	79.5	4.5	Q6DHW4_HUMAN	Q6dhw4 homo sapien
1430	79.5	4.5	Q8SQB6_PIG	Q8sqb6 sus scrofa
1431	79.5	4.5	MYPO_CHICK	Mypo gallus gall
1432	79.5	4.5	Q5WPV1_SHEEP	Q5wpv1 ovis aries
1433	79.5	4.5	Q97XZ7_SULSO	Q97xz7 sulfolobus
1434	79.5	4.5	Q2U8T0_ASPOR	Q2u8t0 aspergillus
1435	79.5	4.5	Q47SW9_THEFY	Q47sw9 thermobifid
1436	79.5	4.5	Q22HC6_CALSA	Q22hc6 caldicellul
1437	79.5	4.5	Q5WRG0_SHEEP	Q5wrg0 ovis aries
1438	79.5	4.5	CYSP4_BRANA	P25251 brassica na
1439	79.5	4.5	Q6GM08_XENLA	Q6gm08 xenopus lae
1440	79.5	4.5	Q28ZX1_DROPS	Q28zx1 drosophila
1441	79.5	4.5	Q4VA91_MOUSE	Q4va91 mus musculu
1442	79.5	4.5	Q8EMV2_OCEIH	Q8emv2 oceanobacil
1443	79.5	4.5	Q1CF48_YERPE	Q1cf48 yersinia pe
1444	79.5	4.5	Q1CAY7_YERPE	Q1cay7 yersinia pe
1445	79.5	4.5	Q66GZ6_YERPS	Q66gz6 yersinia ps
1446	79.5	4.5	Q8ZHN7_YERPE	Q8zhn7 yersinia pe
1447	79.5	4.5	Q93534_XENLA	Q93534 xenopus lae
1448	79.5	4.5	Q2QD20_HUMAN	Q2qd20 homo sapien
1449	79.5	4.5	Q24LN3_CANFA	Q24ln3 canis famil
1450	79.5	4.5	Q7RL88_PLAYO	Q7rl88 plasmodium
1451	79.5	4.5	TPSN_CHICK	Q073895 gallus gall
1452	79.5	4.5	Q76LJ8_COTJA	Q76lj8 coturnix co
1453	79.5	4.5	Q69885_STRCO	Q69885 streptomyce
1454	79.5	4.5	Q4S5U7_TETNG	Q4s5u7 tetraodon n
1455	79.5	4.5	Q3YR25_EHRCJ	Q3yr25 ehrlichia c
1456	79.5	4.5	Q7ZU39_BRARE	Q7zu39 brachydanio
1457	79.5	4.5	TIME_ECOLI	Q047282 escherichia
1458	79.5	4.5	Q3Q5H1_9GAMM	Q3q5h1 shewanella
1459	79.5	4.5	Q5E9Z9_BOVIN	Q5e9z9 bos taurus
1460	79.5	4.5	Q4L8S1_STAHJ	Q4l8s1 staphylococ
1461	79.5	4.5	Q8GDL8_PHOLU	Q8gdl8 photorhabdu
1462	79.5	4.5	Q5V7K4_HALMA	Q5v7k4 haloarcula
1463	79.5	4.5	Q7PSJ8_ANOGA	Q7psj8 anopheles g
1464	79.5	4.5	Q41M22_METBU	Q41m22 methanococc
1465	79.5	4.5	Q86SD2_CIOIN	Q86sd2 ciona intes
1466	79.5	4.5	Q75WK5_ORYLA	Q75wk5 oryzias lat
1467	79.5	4.5	Q4RFH6_TETNG	Q4rfh6 tetraodon n
1468	79.5	4.5	Q4DMH2_TRYCR	Q4dmh2 trypanosoma
1469	79.5	4.5	PECA1_PIG	Q95242 sus scrofa
1470	79.5	4.5	Q6P4H5_HUMAN	Q6p4h5 homo sapien
1471	79.5	4.5	Q388A9_9TRYP	Q388a9 trypanosoma
1472	79.5	4.5	Q8C756_MOUSE	Q8c756 mus musculu
1473	79.5	4.5	Q91YY0_MOUSE	Q91yy0 mus musculu
1474	79.5	4.5	Q4C2C3_TRYCR	Q4c2c3 trypanosoma
1475	79.5	4.5	PMS2_MOUSE	P54279 mus musculu
1476	79.5	4.5	VLDLR_MOUSE	P98156 mus musculu
1477	79.5	4.5	Q4RKK6_TETNG	Q4rkk6 tetraodon n
1478	79.5	4.5	Q73L80_TREDE	Q73l80 treponema d
1479	79.5	4.5	ROBO4_RAT	Q80W87 rattus norv
1480	79.5	4.5	Q26C18_9BACT	Q26c18 flavobacter
1481	79.5	4.5	CSF1R_FELCA	P13369 felis silve
1482	79.5	4.5	Q6PA07_XENLA	Q6pa07 xenopus lae
1483	79.5	4.5	Q1XXB4_CYTJO	Q1xxb4 flavobacter
1484	79.5	4.5	TTF2_HUMAN	Q9uny4 homo sapien
1485	79.5	4.5	Q8OYQ1_MOUSE	Q8oyq1 mus musculu
1486	79.5	4.5	Q8CGB2_MOUSE	Q8cgb2 mus musculu
1487	79.5	4.5	Q4LJS3_9BURK	Q4ljs3 burkholderi
1488	79.5	4.5	Q1BG70_9BURK	Q1bg70 burkholderi
1489	79.5	4.5	Q5AQK4_EMENI	Q5aqk4 emericella
1490	79.5	4.5	Q9GPP6_DROME	Q9gpp6 drosophila
1491	79.5	4.5	Q9VPZ7_DROME	Q9vpz7 drosophila

Right column:

1492	1355	2	Q5TUE1_ANOGA	Q5tue1 anopheles g
1493	1386	2	Q2SH64_HAHCH	Q2sh64 hahella che
1494	1434	2	Q2SPP2_HAHCH	Q2spp2 hahella che
1495	1465	1	MYOM2_HUMAN	P54296 homo sapien
1496	1496	2	Q3KPI9_HUMAN	Q3kpi9 homo sapien
1497	1614	2	Q7RN98_PLAYO	Q7rn98 plasmodium
1498	1670	2	Q7Q2P4_GIALA	Q7q2p4 giardia lam
1499	1838	1	COS5A1_MOUSE	C05a1 mus musculu
1500	2253	2	Q8JV21_9PICO	Q8jv21 ljungan vir

ALIGNMENTS

RESULT 1
SLAF7_HUMAN

ID   SLAF7_HUMAN   STANDARD;   PRT;   335 AA.
AC   Q9NQ25; Q8N6Y8; Q8ND32; Q9NY08; Q9NY23;
DT   24-MAY-2005, integrated into UniProtKB/Swiss-Prot.
DT   01-OCT-2000, sequence version 1.
DT   13-JUN-2006, entry version 39.
DE   SLAM family member 7 precursor (CD2-like receptor activating cytotoxic
DE   cells) (CRACC) (Protein 19A) (CD2 subset 1) (Novel Ly9) (Membrane
DE   protein FOAP-12) (CD319 antigen).
GN   Name=SLAMF7; Synonyms=CS1; ORFNames=UNQ576/PRO1138;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND TISSUE SPECIFICITY.
RX   MEDLINE=21115149; PubMed=11220635; DOI=10.1007/s002510000274;
RA   Boles K.S., Mathew P.A.;
RT   "Molecular cloning of CS1, a novel human natural killer cell receptor
RT   belonging to the CD2 subset of the immunoglobulin superfamily.";
RL   Immunogenetics 52:302-307(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE
RP   SPECIFICITY.
RX   PubMed=11698418;
RA   Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;
RT   "Activation of NK cell-mediated cytotoxicity by a SAP-independent
RT   receptor of the CD2 family.";
RL   J. Immunol. 167:5517-5521(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 3), FUNCTION, AND TISSUE
RP   SPECIFICITY.
RX   MEDLINE=21661458; PubMed=11802771; DOI=10.1042/0264-6021:3610431;
RA   Murphy J.J., Hobby P., Vilarino-Varela J., Bishop B., Iordanidou P.,
RA   Sutton B.J., Norton J.D.;
RT   "A novel immunoglobulin superfamily receptor (19A) related to CD2 is
RT   expressed on activated lymphocytes and promotes homotypic B-cell
RT   adhesion.";
RL   Biochem. J. 361:431-436(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC   TISSUE=Macrophage;
RA   Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,
RA   Naito K., Kawaguchi A.;
RT   "Homo sapiens mRNA for FOAP-12 protein, complete cds.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

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RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
RC   TISSUE=Lymph node;
RG   The German cDNA consortium;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=16710414; DOI=10.1038/nature04727;
RA   Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D.,
RA   Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A.,
RA   Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F.,
RA   McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C.,
RA   Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P.,
RA   Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K.,
RA   Babbage A.K., Bagguley C.L., Bailey J., Beasley H., Bethel G.,
RA   Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D.,
RA   Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G.,
RA   Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J.,
RA   Deadman R., Dunn M., Earthrowl M., Ellington A.G., Errington H.,
RA   Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L.,
RA   Ghori M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J.,
RA   Grafham D.V., Griffiths C., Griffiths-Jones S., Grocock R.,
RA   Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D.,
RA   Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G.,
RA   Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M.,
RA   Kershaw J.K., Kibukawa M., Kimberley A.M., King A., Knights A.J.,
RA   Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M.,
RA   Loveland J., Lovell J., Lush M.J., Lyne R., Martin S.,
RA   Mashreghi-Mohammadi M., Matthews L., Matthews N.S.W., McLaren S.,
RA   Milne S., Mistry S., Moore M.J.F., Nickerson T., O'Dell C.N.,
RA   Oliver K., Palmeiri A., Palmer S.A., Parker A., Patel D., Pearce A.V.,
RA   Peck A.I., Pelan S., Phelps J., Phillimore B.J., Plumb R., Rajan J.,
RA   Raymond C., Rouse G., Saenphimmachak C., Sehra H.K., Sheridan E.,
RA   Shownkeen R., Sims S., Skuce C.D., Smith M., Steward C.,
RA   Subramanian S., Sycamore N., Tracey A., Tromans A., Van Helmond Z.,
RA   Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E.,
RA   Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A.,
RA   Vaudin M., Sulston J.E., Durbin R., Hubbard T., Wooster R., Dunham I.,
RA   Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V., Beck S.,
RA   Rogers J., Bentley D.R.;
RT   "The DNA sequence and biological annotation of human chromosome 1.";
RL   Nature 441:315-321(2006).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 3).
RC   TISSUE=Fetal lung, and Fetal spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [9]
RP   PROTEIN SEQUENCE OF 23-37.
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RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [10]
RP   ALTERNATIVE SPLICING.
RX   PubMed=15368895; DOI=10.1002/eji.200424917;
RA   Lee J.K., Boles K.S., Mathew P.A.;
RT   "Molecular and functional characterization of a CS1 (CRACC) splice
RT   variant expressed in human NK cells that does not contain
RT   immunoreceptor tyrosine-based switch motifs.";
RL   Eur. J. Immunol. 34:2791-2799(2004).
RN   [11]
RP   TISSUE SPECIFICITY, AND SAP-BINDING.
RX   MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
RA   Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA   Bosch J., Terhorst C., Engel P.;
RT   "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT   leukocyte cell-surface receptors.";
RL   Immunogenetics 54:394-402(2002).
CC   -!- FUNCTION: Isoform 1 mediates NK cell activation through a SAP-
CC       independent extracellular signal-regulated ERK-mediated pathway.
CC       May play a role in lymphocyte adhesion. Isoform 3 does not mediate
CC       any activation. SAP can bind the cytoplasmic tail of isoform 1
CC       when phosphorylated in the presence of Fyn (in vitro).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1; Synonyms=19A, CS1-L;
CC         IsoId=Q9NQ25-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9NQ25-2; Sequence=VSP_013781;
CC         Note=No experimental confirmation available;
CC       Name=3; Synonyms=19A24, CS1-S;
CC         IsoId=Q9NQ25-3; Sequence=VSP_013782;
CC   -!- TISSUE SPECIFICITY: Expressed in spleen, lymph node, peripheral
CC       blood leukocytes, bone marrow, small intestine, stomach, appendix,
CC       lung and trachea. Expression was detected in NK cells, activated
CC       B-cells, NK-cell line but not in promyelocytic, B-, or T-cell
CC       lines. The isoform 3 is expressed at much lower level tha isoform
CC       1.
CC   -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC       domain.
CC   -!- CAUTION: Ref.3 (CAB76561) sequence differs from that shown due to
CC       frameshifts.
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DR   EMBL; AF291815; AAK11549.1; -; mRNA.
DR   EMBL; AF390894; AAL26989.1; -; mRNA.
DR   EMBL; AJ271869; CAB76561.1; ALT_FRAME; mRNA.
DR   EMBL; AJ276429; CAB81950.2; -; mRNA.
DR   EMBL; AB027233; BAB61022.1; -; mRNA.
DR   EMBL; AY358512; AAQ88876.1; -; mRNA.
DR   EMBL; AL834424; CAD39085.1; -; mRNA.
DR   EMBL; AL121985; CAC00579.1; -; Genomic_DNA.
DR   EMBL; AL121985; CAH73507.1; -; Genomic_DNA.
DR   EMBL; AL121985; CAH73508.1; -; Genomic_DNA.
DR   EMBL; BC027867; AAH27867.1; -; mRNA.
DR   UniGene; Hs.517265; -.
DR   Ensembl; ENSG00000026751; Homo sapiens.
DR   HGNC; HGNC:21394; SLAMF7.
DR   MIM; 606625; gene.
DR   RZPD-ProtExp; IOH11890; -.
DR   RZPD-ProtExp; W0995; -.
DR   GO; GO:0016020; C:membrane; NAS.
DR   GO; GO:0007155; P:cell adhesion; NAS.

Query Match             100.0%;  Score 1772;  DB 1;  Length 335;
Best Local Similarity   100.0%;  Pred. No. 9.9e-141;
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Matches  335;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL  60

Qy   61  VTIQPEGTIIVTQNRNRERVDFPDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEY  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  VTIQPEGTIIVTQNRNRERVDFPDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEY  120

Qy  121  VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALGQAANESHNGSIL  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALGQAANESHNGSIL  180

Qy  181  PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLIVPLLLSL  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLIVPLLLSL  240

Qy  241  FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  FVLGLFLWFLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA  300

Qy  301  NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI  335
         |||||||||||||||||||||||||||||||||||
Db  301  NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI  335
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RESULT 2
Q3T9A2_MOUSE
ID   Q3T9A2_MOUSE             PRELIMINARY;      PRT;   333 AA.
AC   Q3T9A2;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   27-JUN-2006, entry version 10.
DE   Activated spleen cDNA, RIKEN full-length enriched library,
DE   clone:F830226H19 product:SLAM family member 7, full insert sequence.
GN   Name=Slamf7;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis A., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa A.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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Qy  181  PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL  240
         :|:||.||       .|:|||||| .::.:|  .|::.|.|.:|:.:  .:||.:|: .|:|
Db  178  SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL  237

Qy  241  FVLGLFL---WFLKRERQEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK  296
         |.||.||   |||.:.| .:| ...:|||||    .:|||||
Db  238  FAVLLTIFHTTWIKKRKGCE--EDKKRVDRHQEMDLCPHLEENADYDTIPYTEKRRPE  294

Qy  297  EDPANTVYSTVEIPKKMENPHSLLTMPDTRPLFAYENVI  335
         ||||||||||| :||||| :: :|| .|:|  :|||||
Db  295  EDAPNTFYSTVQIPKVVKSPSSLPAKPLVPRSLSPENVI  333
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RESULT 3
SLAF7_MOUSE
ID   SLAF7_MOUSE   STANDARD;   PRT;   333 AA.
AC   Q8BHK6; Q8BTL2; Q8CJ63; Q8CJ64; Q8CJ65; Q91XA0;
DT   24-MAY-2005, integrated into UniProtKB/Swiss-Prot.
DT   24-MAY-2005, sequence version 2.
DT   27-JUN-2006, entry version 28.
DE   SLAM family member 7 precursor (Leukocyte cell-surface antigen) (Novel
DE   Ly9).
GN   Name=Slamf7;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 2 AND 3).
RC   STRAIN=BALB/c, and C57BL/6; TISSUE=Thymus;
RX   MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
RA   Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA   Bosch J., Terhorst C., Engel P.;
RT   "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT   leukocyte cell-surface receptors.";
RL   Immunogenetics 54:394-402(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RC   STRAIN=C57BL/6J; TISSUE=Aorta, Testis, and vein;
RX   PubMed=16141072; DOI=10.1126/science.112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambeei-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla B., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing Pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD; TISSUE=Activated spleen;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
EMBL; AK172665; BAE43122.1; -; mRNA.
MGI;   MGI:1922595; Slamf7.
RZPD-ProtExp; IOM20087; -.
GO;   GO:0016021; C:integral to membrane; RCA.
InterPro; IPR007110; Ig-like.
PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   333 AA; 37287 MW; 96SA0988E40FC129 CRC64;
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Query Match             46.4%;  Score 822;  DB 2;  Length 333;
Best Local Similarity   49.6%;  Pred. No. 1.4e-60;
Matches  168;  Conservative  58;  Mismatches  103;  Indels  10;  Gaps  3;

Qy    1  MAGSPTCLTIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL  60
         |  |||| ||| .:|||||.|::||||||| ||||: .|.|| :|||||||||||
Db    1  MARFSTYIIFTSVLCQLTVRAASGTLKKVAGALDGSVTFTLNITEIKVDYVVWTFNTFFL  60

Qy   61  VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLLKKNDSGIYYVGCIYSSSLQQPSTQBY  120
         :|: .|| ..:|:.| :|||  ||:.|||.||.|.|||||.|..||:.|:|.|:|||.|
Db   61  AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY  117

Qy  121  VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL  180
         |||.|:.||.||||   ::||:||||||||.||  :|  | ||:|:     .|.:::||
Db  118  VLHVYKGHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQFHDGATL  177
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RA   Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 4).
RC   STRAIN=FVB/N; TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Mediates NK cell activation through a SAP-independent
CC       extracellular signal-regulated ERK-mediated pathway. May play a
CC       role in lymphocyte adhesion (By similarity). Isoform 1 does not
CC       bind SAP (in vitro).
CC   -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC       protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1;
CC         IsoId=Q8BHK6-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q8BHK6-2; Sequence=VSP_013784;
CC       Name=3;
CC         IsoId=Q8BHK6-3; Sequence=VSP_013783, VSP_013784;
CC       Name=4;
CC         IsoId=Q8BHK6-4; Sequence=VSP_013783;
CC         Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Expressed in spleen, lymph node, bone marrow
CC       and testis. Lower levels detected in thymus. Expressed in NK cells
CC       and B-cells.
CC   -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC       domain.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC       frameshift in position 255.
CC   ----
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----
DR   EMBL; AF467909; AAN63158.1; -; mRNA.
DR   EMBL; AF467910; AAN63159.1; -; mRNA.
DR   EMBL; AF467911; AAN63160.1; -; mRNA.
DR   EMBL; AK030135; BAC26801.1; -; mRNA.
DR   EMBL; AK030148; BAC26810.1; -; mRNA.
DR   EMBL; AK040678; BAC30665.1; -; mRNA.
DR   EMBL; AK089525; BAC40914.1; -; mRNA.
DR   EMBL; BC011154; AAH11154.1; ALT_FRAME; mRNA.
DR   Ensembl; ENSMUSG00000038179; Mus musculus.
DR   MGI; MGI:1922595; Slamf7.
DR   RZPD-ProtExp; IOM20087;.
DR   InterPro; IPR007110; Ig-like.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Alternative splicing; Glycoprotein; Immunoglobulin domain; Membrane;
KW   Receptor; Signal; Transmembrane.
FT   SIGNAL        1     22       By similarity.
FT   CHAIN        23    333       SLAM family member 7.
FT                                /FTId=PRO_0000014964.
FT   TOPO_DOM     23    224       Extracellular (Potential).
FT   TRANSMEM    225    245       Potential.
FT   TOPO_DOM    246    333       Cytoplasmic (Potential).
FT   DOMAIN      128    203       Ig-like C2-type.
FT   CARBOHYD     42     42       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD     95     95       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    139    139       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    145    145       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    156    156       N-linked (GlcNAc...) (Potential).
FT   DISULFID    142    212       Potential.
FT   DISULFID    148    192       By similarity.
FT   VAR_SEQ     255    289       Missing (in isoform 3 and isoform 4).
FT                                /FTId=VSP_013783.
FT   VAR_SEQ     312    333       KSPSSLPAKPLVPRSLSFENVI -> RSCPAEHLTCQPLS
FT                                LDHARAQ (in isoform 2 and isoform 3).
FT                                /FTId=VSP_013784.
FT   CONFLICT    118    118       V -> A (in Ref. 1; AAN63158).
FT   CONFLICT    248    248       T -> M (in Ref. 1; AAN63158 and 2).
FT   CONFLICT    253    253       G -> R (in Ref. 1; AAN63159 and 3).
SQ   SEQUENCE   333 AA;  37187 MW;  8D40B823FEBE7129 CRC64;

Query Match             46.0%;  Score 815;  DB 1;  Length 333;
Best Local Similarity   49.3%;  Pred. No. 5.4e-601;
Matches  167;  Conservative   58;  Mismatches  104;  Indels   10;  Gaps    3;

Qy     1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
           ||  | |  |||  ||| |||| |||  | : |  ::|||:||  ||||| |||| ||||||
Db     1 MARFSTYIIFTSVLCQLTVTAASGTLKVVAGALDGSVTFTLNITEIKVDYVVWTFNTFPL 60

Qy    61 VTIQPEGGTIIVTQNRNRERVDPPDGGYSLKLSKLKKNDSGIYYVGIYSSLQQPSTQBY 120
           ::: :||  |: :||:|||||||||  ||| ||| || ||| ||| ||:|:||::|| ||
Db    61 AMVKKDG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy   121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTWKALGQAANESHNGSIL 180
           ||||:  :|:|| |:|:|:||||| |:|:|| || |:||||||:||| |  :  |||| :
Db   118 VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGQGDNQPHDGATL 177

Qy   181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
           |:||||  ||| ||||||||| |||||| | || |||  :   |  |||||: ||||||
Db   178 SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy   241 FVLGLFL----WFLKREROEEYIEBKKRKVDICRETPNICPHSGENTEYDTIPHTNRTLIK 296
           |  || |     |  ::  : |::| :  |   |  ||  | ::::| ||:|| | ::
Db   238 FAVLLTFHTTWIKKGKGCE---EDKKRVDRHQEMPDLCPHLEENADYDTIPYTEKRRPE 294

Qy   297 EDPANTVYSTVEIPKGKMENPHSLLTMPDTPRLFAYENVI 335
           |||.|| |||  |:|  :   |    ||| || |  || ||
Db   295 EDAPNTFVSTVQIPKVVKSPSSLPAKPIVPRSLSFENVI 333


RESULT 4
Q18PI2_MOUSE
ID   Q18PI2_MOUSE   PRELIMINARY;   PRT;   335 AA.
AC   Q18PI2;
DT   25-JUL-2006, integrated into UniProtKB/TrEMBL.
DT   25-JUL-2006, sequence version 1.
DT   25-JUL-2006, entry version 1.
DE   CS1.
GN   Name=Cs1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BXSB/MpJ, NZW/LacJ, NZB/BlNJ, and MRL/MpJ;
RA   Furukawa H., Ono M.;
RT   "Polymorphisms of SLAM family receptor genes.";
```

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RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------
DR   EMBL; AB196819; BAE96322.1; -; mRNA.
DR   EMBL; AB196818; BAE96321.1; -; mRNA.
DR   EMBL; AB196817; BAE96320.1; -; mRNA.
DR   EMBL; AB196816; BAE96319.1; -; mRNA.
SQ   SEQUENCE   335 AA;   37591 MW;   85F00ABDFC8B90A0 CRC64;

Query Match             43.9%;  Score 778.5;  DB 2;  Length 335;
Best Local Similarity   48.8%;  Pred. No. 6.5e-57;
Matches  161;  Conservative  55;  Mismatches 101;  Indels  13;  Gaps   4;

Qy    1  MAGSPTCLTIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL  60
            |:  ||||||||||| |||| :|| ||| |::| ||| ||: : |||:|||:|||||
Db    1  MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVFTLNITEIKVDYVVWTFNTFFL  60

Qy   61  VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSLQQPSTQEY 120
           :||: |: ||: ||: | :|| |||  : |:| ||||:|| ||: |:|||||||||
Db   61  AMVKDKG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy  121  VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  118  VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGGDNQFHDGATL 177

Qy  181  PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
           |:|||||||||||||||||||||||||| ||:|  ::|:|:||::||||:|||||||
Db  178  SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy  241  FVLGLFL----WFLKRERQEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK 296
           || :| |    ||||||| |||||||||||||||||||||||||||||||||||||||
Db  238  FAVLLTIFHTWIKKRKGCE--EDKKRVDRHQEMPDLCPHLEENADYDTIPYTEKRRPE 294

Qy  297  EDPANTVYSTVEIPKKMEN---PHSLLTMP 323
           ||||||||||||||||||   |||||||||
Db  295  EDAPNTFYSTVQIPKVVRSCPAEHHLTCQP 324
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RESULT 5
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Q18PG4_MOUSE
ID   Q18PG4_MOUSE   PRELIMINARY;   PRT;   300 AA.
AC   Q18PG4;
DT   25-JUL-2006, integrated into UniProtKB/TrEMBL.
DT   25-JUL-2006, sequence version 1.
DT   25-JUL-2006, entry version 1.
DE   CS1s.
GN   Name=Cs1s;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MRL/MpJ;
RA   Furukawa H., Ono M.;
RT   "Polymorphisms of SLAM family receptor genes.";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------
DR   EMBL; AB196837; BAE96340.1; -; mRNA.
SQ   SEQUENCE   300 AA;   33431 MW;   9948OA3710BEBC2C CRC64;

Query Match             37.1%;  Score 658;  DB 2;  Length 300;
Best Local Similarity   42.7%;  Pred. No. 8.3e-47;
Matches  141;  Conservative  50;  Mismatches  91;  Indels  48;  Gaps   4;

Qy    1  MAGSPTCLTIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL  60
            |:  ||:| |:||||| |||  :|| ||||:| ||| ||: : |||:|||:|||||
Db    1  MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVFTLNITEIKVDYVVWTFNTFFL  60
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Db    1  MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVFTLNITEIKVDYVVWTFNTFFL  60

Qy   61  VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSLQQPSTQEY 120
           :|| ::| |: | ::|::| || |||| : |:| ||||:|| ||: |:|||||||||
Db   61  AMVKDKG---VTSQSSNKERIVFPDGLYSMKLSQLKKNDSGAYRAEIYSTSSQASLIQEY 117

Qy  121  VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
           ||||| ||| |||| |||||||||| ||| | :| || | ||:|||| : :::| | |
Db  118  VLHVYKHLSRPKVTIDRQSNKNGTCVINLTCSTDQDGENVTYSWKAVGGDNQFHDGATL 177

Qy  181  PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 180
           |:|||||||||||||||||||||: | ||: | ::   ::|:|:||::||||:|||||||
Db  178  SIAWRSGEKDQALTCMARNPVSNSFSTPVFPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

Qy  241  FVLGLFL----WFLKRERQEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILK 240
           ||:| |    |||||||| :||:||    :::|:       |:||:|  |: ::
Db  238  FAVLLTIFHTWIKKRKGCE---EDKKRVDRHQEMPDLCPHLEENADYDTIPYTEKRRPE 237

Qy  297  EDPANTVYSTVEIPKKMEN---PHSLLTMP 323
           || ||:|||:| ||:  :|   |||||  |
Db  295  EDAPNTFYSTVQIPKVVRSCPAEHHLTCQP 323
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RESULT 6
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Q3TBT1_MOUSE
ID   Q3TBT1_MOUSE   PRELIMINARY;   PRT;   328 AA.
AC   Q3TBT1;
DT   11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT   11-OCT-2005, sequence version 1.
DT   27-JUN-2006, entry version 9.
DE   NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched
DE   library, clone:F630222C19 product:CD84 antigen, full insert sequence.
GN   Name=Cd84;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=99279253; PubMed=10349636;  DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
```

RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura R., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagani M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawai J., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashimoto W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=20530911; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RA   Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Kawai J., Kojima M., Konno M., Murata M., Nakamura M., Ninomiya N.,
RA   Nishiyori H., Nomura K., Ohno M., Sakazume M., Sano H., Sasaki D.,
RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---
DR   EMBL; AK171067; BAE42226.1; -; mRNA.
DR   MGI; MGI:1336885; Cd84.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig_sub.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE   328 AA;   37307 MW;   95E1FA3C07E0FB77 CRC64;

Query Match   20.8%; Score 368; DB 2; Length 328;
Best Local Similarity   30.5%; Pred. No. 2.7e-22;
Matches 105; Conservative 63; Mismatches 134; Indels 42; Gaps 14;

Qy   11 IYILWQLTGSAASGPVKE---LVGSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQP- 65
               |::|| ::| : :| | ||:: : | : | ::| :|| | : : |
Db   8 IWFLCLQTWSRAAGKDADPMVWNGILGESVTFLLNIQEPKKIDNIAWT-SQSSVAFIKPG 66

Qy   66 -EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYVGYISSSLQQPSTQEYVLHV 124
               |::| || :::| |: | :| : : ::| | :   :| :
Db   67 VNKAEVTITQGTYKGRIEIIDQKYDLVIRDLRMEDAGTYKADINEEN-EETITKIYYLHI 125

Qy   125 YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISW 184
               | | :: || | : | | | || :| || : : :   : | :
Db   126 YRRLKTPKITQSLISSLNNTCNITLTCSVEKEKDVTYSWSPFGEKSN----VLQIVH 179

Qy   185 RWGESDMTFICVARNPVSRNFSSPILARKLCEGA-------ADDPDSSMVLLCLLLVPLL 237
               ||| | | | | :: | | : | || : :| | || :|
Db   180 SPMDQKLTYTCTAQNPVS-NSSDSVTVQQPCTDTPSFHPRHAVLPGGLAVLFLLILPML 238

Qy   238 LSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP-NICPHSGENTE--YDTPHTNRT 293

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Db     239  APLFRL------YKRRRDRIVLED-----DVSKKTVYAVVSRNAQPTESRIYDEIPQSKML  288
                  |||    |  :  |||:     |:  ::|       :  :.|     ||  |||:|
Qy     294  ILKEDPANTVVSTVEIPKKMENPHSLLTMPD--TPRLFAYENVI  335
                  ||||  |:|::|::.:||:  :  .  ||:|  ||:||
Db     289  SCKEDPVTTIYSSVQLSEKMKETN----MKDRSLPKALGNEIVV  328

RESULT 7
Q18PI6_MOUSE
ID   Q18PI6_MOUSE    PRELIMINARY;    PRT;   329 AA.
AC   Q18PI6;
DT   25-JUL-2006, integrated into UniProtKB/TrEMBL.
DT   25-JUL-2006, sequence version 1.
DT   25-JUL-2006, entry version 1.
DE   CD84.
GN   Name=Cd84;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BXSB/MpJ, NZB/B1NJ, and MRL/MpJ;
RA   Furukawa H., Ono M.;
RT   "Polymorphisms of SLAM family receptor genes.";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AB196815; BAE96318.1; -; mRNA.
DR   EMBL; AB196813; BAE96316.1; -; mRNA.
DR   EMBL; AB196812; BAE96315.1; -; mRNA.
SQ   SEQUENCE   329 AA;  37378 MW;  B3BF45FEA7B00FB6 CRC64;

Query Match             20.6%;  Score 364.5;  DB 2;  Length 329;
Best Local Similarity   30.5%;  Pred. No. 5.4e-22;
Matches  105;  Conservative   62;  Mismatches 136;  Indels  41;  Gaps  14;

Qy      11  IYILMQLTGSAASGPVKE---LVGSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQP-  65
                | |:    |:.|:|:||||     :|| |:|  |  .|  |||:  |  :|  |  :  ||
Db       8  IWFLCLQTWSEAAGKDADPMVMNGILGESVTFLLNIQEPKKIDNIAWT-SQSSVAFIKPG  66

Qy      66  -EGGTIIVTQNRNRERVDFPDPGGYSLKLSKLKKNDSGIYYVGIYSSLQQPSTQEYVLHV  124
                 :||    | |::|::||||     |:|| :||   | :|| || :|||.:| |::|:||:|
Db      67  VNKAEVTITQGTYKGRIEIIDQKYDLVIRDLRMEDAGTYKADINEEN-EETITKIYYLHI  125

Qy     125  YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTWKALGQAANESHNGSILPISW  184
                     |:.||:|   |::: |  |  | || :|     | ||: :|    : |::  | :||
Db     126  YRRLKTPKITQSLISSLNNTCNITLTCSVEKEBKDVTYSWSPFGEKSN-----VLQIVH  179

Qy     185  RWGESDMTFICVARNPVSRNFSSPIIARKLCEGA-------ADDPDSSMVLLCLLLVPLL  237
                  | | ::|  :|  | || | .|:|   | |  |        :  | |:||:.|||.||:||
Db     180  SPMDQKLTYTCTAQNPVS-NSSDSVTVQQPCTDTPSFHPRHAVLPGGLAVLFLLILIPML  238

Qy     238  LSLFVLGLFLMFLKRERQEBYIEBKKRVDICRETP-NICPHSGENTB--YDTIPHTNRT  293
                      |:  | ||:|: :|     |:||   ||| |  :      |: || |||  |  |:
Db     239  AFLFRL------YKRRRDRIVLEAD--DVSKKTVYAVVSRNAQPTESRIYDEIPQSKML  289

Qy     294  ILKEDPANTVVSTVEIPKKMENPHSLLTMPD--TPRLFAYENVI  335
                  ||||  |:|::|::.:||:  :  .  ||:|  ||:||
Db     290  SCKEDPVTTIYSSVQLSEKMKETN----MKDRSLPKALGNEIVV  329

RESULT 8
O15430_HUMAN
ID   O15430_HUMAN    PRELIMINARY;    PRT;   328 AA.
AC   O15430; Q8WLP1;
DT   01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT   01-JAN-1998, sequence version 1.
DT   25-JUL-2006, entry version 43.
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DE   Leukocyte antigen CD84 (CD84 antigen) (Leukocyte antigen) (MAX.3 cell
DE   surface antigen precursor) (Leukocyte differentiation antigen CD84
DE   isoform CD84C).
GN   Name=CD84; ORFNames=RP11-528G1.3-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=9754416; PubMed=9310491;
RA   de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
RT   "CD84 leukocyte antigen is a new member of the Ig superfamily.";
RL   Blood 90:2398-2405(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Lad H.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86188202; PubMed=3008886;
RA   Andreesen R., Bross K.J., Osterholz J., Emmrich F.;
RT   "Human macrophage maturation and heterogeneity: analysis with a newly
RT   generated set of monoclonal antibodies to differentiation antigens.";
RL   Blood 67:1257-1264(1986).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021:3460729;
RA   Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.;
RT   "Characterization of MAX.3 antigen, a glycoprotein expressed on mature
RT   macrophages, dendritic cells and blood platelets: identity with
RT   CD84.";
RL   Biochem. J. 346:729-736(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RA   Palou E., Sole J., Pirotto F., Gaya A.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   ---
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CC   ---
DR   EMBL; U82988; AAB84364.1; -; mRNA.
DR   EMBL; AL138930; CAI15158.1; -; Genomic_DNA.

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DR   EMBL; AJ223324; CAA11264.1; -; mRNA.
DR   EMBL; AF054815; AAF21721.1; -; mRNA.
DR   EMBL; BC020063; AAH20063.1; -; mRNA.
DR   UniGene; Hs.398093; -.
DR   Ensembl; ENSG00000066294; Homo sapiens.
DR   RZPD-ProtExp; IOH11227; -.
DR   RZPD-ProtExp; RZPD0834H0132; -.
DR   RZPD-ProtExp; S0296; --.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0006952; P:defense response; TAS.
DR   GO; GO:0007156; P:homophilic cell adhesion; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig_sub.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Repeat; Signal.
SQ   SEQUENCE   328 AA;  36871 MW;  6C9A89206A6D0344 CRC64;

Query Match             20.5%;  Score 362.5;  DB 2;  Length 328;
Best Local Similarity   31.5%;  Pred. No. 8e-22;
Matches   107;  Conservative   55;  Mismatches  143;  Indels   35;  Gaps    10;

Qy     14 LWQL-----TGSAASGPVKELV---GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
             ||         ||     :|||      :|||||||        |:::|: |||||
Db      6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP 65

Qy     65 PEGGT---IIVTQNRNRERVDFPDDGGYSLKLKSKLKKNDSGIYVYGIYSSSLQQPSTQEYV 121
            |||       ||        ||    |:|:  |:|:|| ::|||| | |     :|| |:
Db     66 GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125

Qy    122 LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGGEDVIYTWKALGQAANESHNGSILP 181
            | |  || |  | :|:  |:| || ||    |||  |: |||  ||| ::|:| ||| |
Db    126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPLGE------EGNVLQ 179

Qy    182 ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDS-----SMVLLCLLLVP 235
            :|||| |||  ||  |:|  |||   |     |||   ||        ||||| |:|:
Db    180 IFQTPEDQELTYTCTAQNPVSNN-SDSISARQLCADIAMGFRTHTGLLSVLAMFLLVL 238

Qy    236 LLLSLFVLGLFLWFLKRERQEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
            |||:| |:||| || |  :  ||          ||    |  || || |    ||:||
Db    239 ILSSVFLFRLF-----KRRQDAASKKTIYTYIMASRNTQP--AESRIYDEILQSKVLPS 290

Qy    296 KEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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Db    291 KEEPVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328
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RESULT 9
Q92178_MOUSE
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ID   Q92178_MOUSE    PRELIMINARY;    PRT;    329 AA.
AC   Q92178;
DT   01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1999, sequence version 1.
DT   27-JUN-2006, entry version 34.
DE   CD84 leukocyte antigen (NOD-derived CD11c +ve dendritic cells cDNA,
DE   RIKEN full-length enriched library, clone:F630108I06 product:CD84
DE   antigen, full insert sequence).
GN   Name=Cd84; Synonyms=CD84;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peritoneum;
RX   MEDLINE=99180614; PubMed=10079287; DOI=10.1007/s002510050490;
RA   de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
RA   Engel P.;
RT   "Molecular cloning, characterization, and chromosomal localization of
RT   the mouse homologue of CD84, a member of the CD2 family of cell
RT   surface molecules.";
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RL   Immunogenetics 49:249-255(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Methods Enzymol. 303:19-44(1999).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlested C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   PubMed=16141073; DOI=10.1126/science.1112009;
RG   RIKEN Genome Exploration Research Group, and Genome Science Group
RG   (Genome Network Core Team) and the FANTOM Consortium;
RT   "Antisense Transcription in the Mammalian Transcriptome.";
RL   Science 309:1564-1566(2005).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
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RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reid D.J., Ring J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD.
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD.
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka A., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NOD;
RA   Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA   Arakawa T., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA   Hori F., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA   Kawai J., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

RA   Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---
DR   EMBL; AF043445; AAD02273.1; -; mRNA.
DR   EMBL; AK154834; BAE32863.1; -; mRNA.
DR   UniGene; Mm.259115; -.
DR   Ensembl; ENSMUSG00000038147; Mus musculus.
DR   MGI; MGI:1336885; Cd84.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig_sub.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
SQ   SEQUENCE 329 AA; 37345 MW; 43BB1A5AF1989E0 CRC64;

Query Match   20.5%; Score 362.5; DB 2; Length 329;
Best Local Similarity 30.5%; Pred. No. 8e-22;
Matches 105; Conservative 62; Mismatches 136; Indels 41; Gaps 14;

Qy   11 IYIIWQLTGSAASGPVKELV---GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQP- 65
               :||:::||||:|::|| ::|:||::|| ||:|::|::| :::: |::|||
Db   8 IWFLCLQTWSEAAGKDADPVVMNGILGESVTFLLNIQEPKKIDNIAWT-SQSSVAFIKPG 66

Qy   66 -EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYVGIYSSSLQQPSTQEYVLHV 124
            ||||:|||::::|||:| |: |:::|||::||:|||||||||:::|::::||::||:
Db   67 VNKAEVTITQGTYKGRIEIIDQKYDLVIRDLRMEDAGTYKADINEEN-EETITKIYLHI 125

Qy   125 YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISW 184
               ||:||:| ||| |||:| |:|:| :||||||||::||: :|| ||:||:|::
Db   126 YRRLKTPKITQSLISSLNNTCNITLTCSVBKEEKDVTYSWSPFGEKSN-----VLQIVH 179

Qy   185 RWGESDMTFICVARNPVSRNFSSPILARKLCEGA-------ADDPDSSMVLLCLLLVPLL 237
               : |::::|:||:|||||| ||::: || :|| ::||:|:| ::|:::|
Db   180 SPMDQKLTYTCTAQNPVS-NSSDSVTVQQPCTDTPSFHPRHAVLPGGLAVLFLLILIPML 238

Qy   238 LSLFVLGLFLWFLKRERQEYIEEKKRVDICRETP-NICPHSGENTE---YDTIPHTNRT 293
              :|||:||:|||||:|::|::||||||:||||:|||| :|||::|||: ||::||:|||
Db   239 AFLFRL------YKRRRDRIVLEAD---DVSKKTVYAVVSRNAQPTESRIYDEIPQSKML 289

Qy   294 ILKEDPANTVYSTVEIPKKMENPHSLLTMPD--TPRLFAYENVI 335
              :|||:||||||||:|||:||::||::||::||| :|||:|:||:|
Db   290 SCKKDPVTTIYSSVQLSEKMKETN----MKDRSLPKALGNEIVV 329

RESULT 10
Q18PI7_MOUSE
ID   Q18PI7_MOUSE   PRELIMINARY;   PRT;   329 AA.
AC   Q18PI7;
DT   25-JUL-2006, integrated into UniProtKB/TrEMBL.
DT   25-JUL-2006, sequence version 1.
DT   25-JUL-2006, entry version 1.
DE   CD84.
GN   Name=Cd84;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NZW/LacJ;
RA   Furukawa H., Ono M.;
RT   "Polymorphisms of SLAM family receptor genes.";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; AB196814; BAE96317.1; -; mRNA.
SQ   SEQUENCE 329 AA; 37377 MW; B3BF45FEAF128596 CRC64;

Query Match   20.3%;   Score 360.5; DB 2;   Length 329;
Best Local Similarity 30.2%;   Pred. No. 1.2e-21;
Matches 104; Conservative 63; Mismatches 136; Indels 41; Gaps 14;

Qy   11 IYILWLGTGSAASGPVKE--LVGSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQP- 65
            :| : || :| ||||| :||||:| :: |::|:||||:||||||||||:
Db   8 IWFLCLQTWSEAAGKDADPMVMNGIIGESVTFLLNIQEPKKIDNIAWT-SQSSVAFIKPG 66

Qy   66 -EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV 124
          ||||||:|||||||||||||||| |:|||:|||||||||||||||||:|::| :||:|||
Db   67 VNKAEVTITQGTYKGRIEIIDQKYDLVIRDLRMEDAGTYKADINEEN-EETITKIYYLHI 125

Qy   125 YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISW 184
          |||||||||||||||||||||||||||:|||:||||||||||||||||||||||||| ||
Db   126 YRRLKTPKITQSLISSLNNTCNITLTCSVEKEEKDVTYSWSPFGEKSN-----VLQIVH 179

Qy   185 RWGESDMTFICVARNPVSRNFSSPILARKLCEGA------ADDPSSMVLLCLLLVPLL 237
          |||||||||||||||||||||||||||||||:||| ::||:::|::||||:||:
Db   180 IFQTPEDQELYTCTAQNPVSNN-SDSISARQLC------EYIEEKKRV-DICRETPNICPHSGENTEY 238

Qy   238 LSLFVLGLFLMFLKRERQEEYIEEKKRVDICRETP-NICPHSGENTE--YDTIPHTNRT 293
          |:|:: ||| | ::| ||||||||||||||:   :: | :|||||||||
Db   239 AFLFRL------YKRRRDRIVLEAD---DVSKKTVYAVVSRNAQPESRIYDEIPQSKML 289

Qy   294 ILKEDPANTVYSTVEIPKKMENPHSLLTMPD--TPRLFAYENVI 335
          ||||||||||||||||||||||||||||||| |||||||||:
Db   290 SCKKDPVTTIYSSVQLSEKMKETN----MKDRSLPKALGNEIVV 329

RESULT 11
Q8WWI8_HUMAN
ID   Q8WWI8_HUMAN   PRELIMINARY;   PRT;   339 AA.
AC   Q8WWI8;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   27-JUN-2006, entry version 27.
DE   Leukocyte differentiation antigen CD84 precursor (CD84 antigen)
DE   (Leukocyte antigen).
GN   Name=CD84; ORFNames=RP11-528G1.3-002;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gaya A.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RA   Lad H.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ---
DR   EMBL; Y12632; CAA73181.1; -; mRNA.
DR   EMBL; AL138930; CAI15159.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000066294; Homo sapiens.
DR   RZPD-ProtExp; IOH11227; -.
DR   RZPD-ProtExp; RZPDo834H0132; -.
DR   RZPD-ProtExp; S0296; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig_sub.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Repeat; Signal.
FT   SIGNAL   1   21   Potential.
FT   CHAIN   22   339   leukocyte differentiation antigen CD84.
SQ   SEQUENCE   339 AA; 38082 MW; E78D5CAC8D3604 CRC64;

Query Match   20.3%;   Score 359; DB 2;   Length 339;

Best Local Similarity 31.6%;   Pred. No. 1.6e-21;
Matches 111; Conservative 51; Mismatches 143; Indels 46; Gaps 12;

Qy   14 LWQL----TGSAASGPVKELV--GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
          | : | :|| ||| :| |:| | |:|:| :| |::|:||||:||||||||
Db   6 LWILLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAVTP 65

Qy   65 PEGGT---IIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV 121
          | :   :| ::||||||||||||| |:|: :||||||||||||||||:|:| |||||
Db   66 GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125

Qy   122 LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILP 181
          |:| :|||||:|| |||:||||||||||| | ||||||| :| : | | ::|| ||
Db   126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKVTYNWSPLGE------EGNVLQ 179

Qy   182 ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSM------VLLCLLLV 234
          |: | |||||||||:||||| : :| | |:| : | :::: : |:||| |
Db   180 IFQTPEDQELYTCTAQNPVSNN-SDSISARQLC-----ADIAMGFRTHHTGLLSVLAM 232

Qy   235 PLLSLFVLGLFLWFLKRERQ---------EEYIEEKKRV-DICRETPNICPHSGENTEY 284
          || ::: || | : |: | | ||||| |||||||||||||||||:|
Db   233 FFLLVLILSSVFLFRLFKRRQGSCLNTFTKNPYAASKKTIYTYIMASRNTQP--AESRIY 290

Qy   285 DTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
          :|||||||:|||||||||||||||:||||||:||||||||||||||||||:
Db   291 DEILQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 339

RESULT 12
Q6NZB6_MOUSE
ID   Q6NZB6_MOUSE   PRELIMINARY;   PRT;   645 AA.
AC   Q6NZB6;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   18-APR-2006, entry version 13.
DE   Ly9 protein (Fragment).
GN   Name=Ly9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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CC   --
DR   EMBL; BC066212; AAH66212.1; -; mRNA.
DR   Ensembl; ENSMUSG00000004707; Mus musculus.
DR   MGI; MGI:96885; Ly9.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR013151; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig_sub.
DR   InterPro; IPR013106; Ig_V-set.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF07686; V-set; 1.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
FT   NON_TER   1   1
SQ   SEQUENCE   645 AA; 71884 MW; 316EF183DFD510BB CRC64;

Query Match   20.2%; Score 358.5; DB 2; Length 645;
Best Local Similarity   27.9%; Pred. No. 4.1e-21;
Matches 119; Conservative 51; Mismatches 138; Indels 119; Gaps 16;

Qy   14 LWQL-TGSA---ASGPVKELVGSVGGAVTFPLKSK-VKQVDSIVWTFNTTPLVTIQPEG   67
           :: :   ::: ::   : :   ::   ::   ::   :: :::::
Db   229 IWQFCTGASRRKTAAG--KTVVGILGEPVTLPLEFRATRATKNVVWVFNTS--VISQERR 284

Qy   68 GTIIVTQNR-----NRERVDFPDGGYSLKLSKLKNDSGIYYVGYISSSLQQPSTQEYVL 122
           ::   :   : :: : : ::: : ::::   : :::   :: :
Db   285 GAATADSRRKPKGSEERRVRTSDQDQSLKISQLKMEDAGPYHAYVCSEASRDPSVRHFTL 344

Qy   123 HVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPI 182
           ::::   ::::   :   : :::   : ::::: ::::::::::::::::::::
Db   345 LVYKRLEKPSVTKSPVHMMNGICEVVLTCSVDGGGNNVTYTWMPLQNKAVMSQGKSHLNV 404

Qy   183 SWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLIVPLLLSLFV 242
           ::::::: :   :::::::   : : :::: :   :::   ::   ::
Db   405 SWESGEHLPNFTCTAHNPVS-NSSSQFSSGTICSG---PERNKRFWLLLLLVLLLLMLI 459

Qy   243 LGLFLWFLKRE-------RQEEYIEE-----------------KKRVDICRETPNICP- 276
           :::::::::::   :::::::   ::::: :::   ::
Db   460 GGCFILRKKKQCSSLATRYRQAEVPAEIPETPTGHGQFSVLSQRYKKLDMSAKTTRHQPT 519

Qy'   277 ------------------HSGENTE----YDTIPHTN------------------- 291
                             :: :::   :::: :
Db   277 ------------------------------ADIAMGFRTHTGLLSVLAM------- 232

Qy   292 RTIL--KEDPANTVYSTVEIPKK-MENPHSLLTMPDTP 326
           ::   :::::::::: :::: ::::::::::::::
Db   520 PTSDTSSESSATTEEDDEKTRMHSTANSRNQVYDLVTHQDIAHALAYEGQVEYEAITPYD 579

Qy   327 RLFAYEN 333
          ::::::
Db   580 KVDGSMDEEDTAYIQVSLNVQGETPLPQKKEDSNTIYCSVQKPKKTAQTPQQDAESPETP 639

Db   640 ---TYEN 643

RESULT 13
Q9UIB8_HUMAN
ID   Q9UIB8_HUMAN   PRELIMINARY;   PRT;   345 AA.
AC   Q9UIB8;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   27-JUN-2006, entry version 30.
DE   Leukocyte differentiation antigen CD84 isoform CD84a (CD84 antigen)
DE   (Leukocyte antigen).
GN   Name=CD84; ORFNames=RP11-528G1.3-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.

RA   Palou E., Sole J., Pirotto P., Gaya A.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Lad H.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC   --
DR   EMBL; AF054816; AAF21722.1; -; mRNA.
DR   EMBL; AL138930; CAI15160.1; -; Genomic_DNA.
DR   Ensembl; ENSG00000066294; Homo sapiens.
DR   HGNC; HGNC:1704; CD84.
DR   LinkHub; Q9UIB8;
DR   RZPD-ProtExp; IOH11227; -.
DR   RZPD-ProtExp; RZPDo834H0132; -.
DR   RZPD-ProtExp; S0296; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig_sub.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   345 AA; 38782 MW; DA06BC5A682E62DE CRC64;

Query Match   20.2%; Score 358; DB 2; Length 345;
Best Local Similarity   30.8%; Pred. No. 2e-21;
Matches 110; Conservative 52; Mismatches 143; Indels 52; Gaps 11;

Qy   14 LWQL----TGSAASGPVKELV---GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
           ::::   : :::: :::   :   : :::::::::::::::::::::
Db   6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP 65

Qy   65 PEGGT---IIVTQNRNRERVDFPDGGYSLKLSKLKNDSGIYYVGYISSSLQQPSTQEYV 121
           :   : :: :::   :::: :   :: : : :::   : ::: :::::
Db   66 GDSETAPVVTVTHRNYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125

Qy   122 LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILP 181
           ::::::::::::   : ::: ::: :::::::::::::::::::::::::::::: :
Db   126 LQIYRRLGKPITQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPLGE------EGNVLQ 179

Qy   182 ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSM-----VLLCLLLV 234
           ::::::: :   ::::: :::   ::: ::::   :   :::
Db   180 IFQTPEDQELTYTCTAQNPVSNN-SDSISARQLC-----ADIAMGFRTHTGLLSVLAM 232

Qy   235 PLLLSLFVLGLFLWFLKRERQEEYIEEKKRVDICRETP-----------NICPHS 278
           :::::::   :: : ::::::::   ::::: :::
Db   233 FFLVLILSSVFLFRLFKRRQGRIFPEGSCLNTFTKNPYAASKKTIYTYIMASRNTQP-- 290

Qy   279 GENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
           :::::: :::   : :: :: ::::: ::: :   : :: :::: :::::
Db   291 AESRIYDEIIQSKVLPSKEEPVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 345

RESULT 14
Q6FHA8_HUMAN
ID   Q6FHA8_HUMAN   PRELIMINARY;   PRT;   328 AA.
AC   Q6FHA8;
DT   19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2004, sequence version 1.
DT   13-JUN-2006, entry version 10.
DE   CD84 protein (Fragment).
GN   Name=CD84;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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CC ---
DR EMBL; CR541847; CAG46645.1; -; mRNA.
DR Ensembl; ENSG00000066294; Homo sapiens.
DR RZPD-ProtExp; IOH11227; -.
DR RZPD-ProtExp; RZPDo834H0132; -.
DR RZPD-ProtExp; SO296; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig_sub.
DR SMART; SM00409; IG; 1.
KW Immunoglobulin domain.
FT NON_TER   328   328
PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE   328 AA; 36861 MW; 6CA8BDD45BD0344 CRC64;

Query Match   20.0%; Score 354.5; DB 2; Length 328;
Best Local Similarity   31.2%; Pred. No. 3.8e-21;
Matches 106; Conservative 55; Mismatches 144; Indels 35; Gaps 10;

Qy   14 LWQL----TGSAAASGPVKELV--GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
         |:|| ||| |: : | || | |||: :| |:| || || | ::|
Db   6 LWILLLCLQTWPEAAGKDSEIFTVNGILGESVTFPVNIQEPRQVKIIAWTSKTSVAYVTP 65

Qy   65 PEGGT---IIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYV 121
         |:||| | ||:::: | :| |: ||:| | | |:||||||:|||:|||||||||||||
Db   66 GDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRYN 125

Qy 122 LHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTWKALGQAANESHNGSILP 181
         | |:|| |: | | | | || ||| || :||| | |::||||||:||:||: |||||
Db 126 LQIYRLGKPKITQSLMASVNSTCNVTLTCSVEKEKQNVTYNWSPLGE------EGNVLQ 179

Qy 182 ISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDS------SMVLLCLLLVP 235
         | :|| | :|:: | :|: |:|| | :|:: : |:   :|:|:::||||
Db 180 IFQTPEDQELYTCTAQNPVSNN-SDSISARQLCADIAMGPRTHHTGLLSVLAMFFLLVL 238

Qy 236 LLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTIL 295
         ||:| ||||:||| |:   : :| :| | | :||:| | :| | :|
Db 239 ILSSVFLFRLF------KRRQDAASKKTIYTYIMASRNTQP--AESRIYDEILQSKVLPS 290

Qy 296 KEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
         |||: |||| || | :|| || | :| | ||| |
Db 291 KEESVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328

RESULT 15
Q7TMP7_MOUSE
ID   Q7TMP7_MOUSE   PRELIMINARY;   PRT;   649 AA.
AC   Q7TMP7;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   18-APR-2006, entry version 14.
DE   Ly9 protein (Fragment).
GN   Name=Ly9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---
DR   EMBL; BC055380; AAH55380.1; -; mRNA.
DR   HSSP; P08921; 1HNG.
DR   Ensembl; ENSMUSG00000004707; Mus musculus.
DR   MGI; MGI:96885; Ly9.
DR   GO; GO:0005615; C:extracellular space; RCA.
DR   GO; GO:0016021; C:integral to membrane; RCA.
DR   InterPro; IPR013151; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig_sub.
DR   InterPro; IPR013106; Ig_V-set.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF07686; V-set; 1.
DR   SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
FT   NON_TER   1   1
SQ   SEQUENCE   649 AA; 72415 MW; AD6A09381C063B34 CRC64;

Query Match   20.0%; Score 354.5; DB 2; Length 649;
Best Local Similarity   27.6%; Pred. No. 9e-21;
Matches 118; Conservative 52; Mismatches 138; Indels 119; Gaps 16;

Qy   14 LWQL-TGSA----ASGPVKELVGSVGGAVTFPLKSK-VKQVDSIVWTFNTTPLVTIQPEG 67
         |:|| ||| ||| || || | | ||||:| | :||:|: || ||: : |
Db 233 IWQFCTGASRRKTAAG--KTVVGILGEPVTLPLEFRATRATKNVWVVFNTS--VISQRRR 288

Qy   68 GTIIVTQNR------NRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVL 122
         | :| |:: ||| :| | || ||:| | |:| | |::||||||:||||||| |
Db 289 GAATADSRRKPKGSEERRVRTSDQDQSLKISQLKMBDAGPYHAYVCSEASRDPSVRHFTL 348

Qy 123 HVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEBDVIYTWKALGQAANESHNGSILPI 182
         | |: | | | | | :| | ||| || ::|||| |::|| |: |:| | ::|:|
Db 349 LVYKRLEKPSVTKSPVHMMNGICEVVLTCSVDGGGNNVTYTMPLQNKAVMSQGKSHLNV 408

Qy 183 SWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFV 242
         :|| | ||:: | |:| :|: |:|| |:||| |||||||::|||||:|| |||::|
Db 409 SWESGEHLPNFTCTAHNPVS-NSSSQFSSGTICSG----PERNKRFWLLLLLLLLMLI 463

Qy 243 LGLFLWFLKRE------RQEEYIE---------------------KKRVDICRETPNICP- 276
         |||:||| |:| |:|: | ||||| || ||||
Db 464 GGYFILRKKKQCSSLATRYRQAEVPAEIPETPTGHGQFSVLSQRYEKLDMSAKTTRHQPT 523

Qy 277 ------------------HSGENTE---YDTIPHTN 291
                           :| |:|: |||:||||
Db 524 PTSDTSESSATTEEDDEKTRMHSTANSRNQVVDLVHQDIAHALAVBGQVEYEAITPYD 583

Qy 292 ------------------RTIL--KEDPANTVYSTVEIPKK-MENPHSLLTMPDTP 326
                           :|:| |||||| |||| |:||:| :||||||||| |||
Db 584 KVDGSMDEEGMAYIQVSLNVQGETPLPQKKEDSNTIYCSVQKPKKTAQTPQQDAESPETP 643

Qy 327 RLFAYEN 333
         |||||:|
Db

us-10-063-549-46.spdi.rup

Db   644 ---TYEN 647

Search completed: March 29, 2007, 02:34:47
Job time : 409 secs

OM protein - protein search, using sw model
Run on: March 29, 2007, 02:20:37 ; Search time 99 Seconds
                                          (without alignments)
                                          1655.825 Million cell updates/sec

Title: US-10-063-549-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTLIYILWQLTGS..........PHSLLTMPDTPRLFAYENVI 335
Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2782304
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   A_Geneseq_200701:*
               1: geneseqp1980s:*
               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*
               11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                      SUMMARIES

No.   Score Match Length DB ID   Description
RESULT 1
ID   AAY66701 standard; protein; 335 AA.
DE   Membrane-bound protein PRO1138.
PN   WO9963088-A2.
PD   09-DEC-1999.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 1772; DB 3; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 2
ID   AAY70431 standard; protein; 335 AA.
DE   Human cell surface immunomodulator-1 (CSIMM-1).
PN   WO200011150-A1.
PD   02-MAR-2000.
PA   (INCY-) INCYTE PHARM INC.
       Query Match   100.0%;   Score 1772; DB 3; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 3
ID   AAY44609 standard; protein; 335 AA.
DE   Human myocardium protein-7.
PN   WO9967387-A2.
PD   29-DEC-1999.
PA   (MILL-) MILLENNIUM PHARM INC.
       Query Match   100.0%;   Score 1772; DB 3; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 4
ID   AAU29119 standard; protein; 335 AA.
DE   Human PRO polypeptide sequence #96.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 1772; DB 4; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 5
ID   AAB87548 standard; protein; 335 AA.
DE   Human PRO1138.
PN   WO200116318-A2.
PD   08-MAR-2001.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 1772; DB 4; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 6
ID   AAB47321 standard; protein; 335 AA.

DE   APEX-1.
PN   WO20014 6260-A2.
PD   28-JUN-2001.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
       Query Match   100.0%;   Score 1772; DB 4; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 7
ID   AAB65224 standard; protein; 335 AA.
DE   Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 1772; DB 4; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 8
ID   ABG95873 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2002119130-A1.
PD   29-AUG-2002.
PA   (GETH) GENENTECH INC.
       Query Match   100.0%;   Score 1772; DB 5; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 9
ID   ABU58495 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003027272-A1.
PD   06-FEB-2003.
       Query Match   100.0%;   Score 1772; DB 6; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 10
ID   ABU88043 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003032127-A1.
PD   13-FEB-2003.
       Query Match   100.0%;   Score 1772; DB 6; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 11
ID   ABU84358 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003032112-A1.
PD   13-FEB-2003.
       Query Match   100.0%;   Score 1772; DB 6; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 12
ID   ABR66232 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003027278-A1.
PD   06-FEB-2003.
       Query Match   100.0%;   Score 1772; DB 6; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 13
ID   ABR65622 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003036159-A1.
PD   20-FEB-2003.
       Query Match   100.0%;   Score 1772; DB 6; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 14
ID   ABU99562 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003040070-A1.
PD   27-FEB-2003.
       Query Match   100.0%;   Score 1772; DB 6; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 15
ID   ABU58039 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003027163-A1.
PD   06-FEB-2003.
       Query Match   100.0%;   Score 1772; DB 6; Length 335;
       Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 16
ID   ABU59117 standard; protein; 335 AA.

DE   Novel human secreted or transmembrane protein PRO1138.
PN   US2002133252-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 17
ID   ABU82629 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003032023-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 18
ID   ABU82801 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003032113-A1.
PD   13-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 19
ID   ABU89922 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003036147-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 20
ID   ABR68171 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003027264-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 21
ID   ABU60548 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein, #100.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 22
ID   ABU96224 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003036144-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 23
ID   ABU92655 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003036149-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 24
ID   ABO08732 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003044923-A1.
PD   06-MAR-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 25
ID   ABO02784 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003040062-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 26
ID   ABR74938 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN   US2003040056-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 27
ID   ABR94700 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003044926-A1.
PD   06-MAR-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 28
ID   ABU13930 standard; protein; 335 AA.
DE   Human PRO1138 polypeptide.
PN   US2002103125-A1.
PD   01-AUG-2002.
PA   (GETH) GENENTECH LTD.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 29
ID   ABU85673 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 30
ID   ABU98833 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003013153-A1.
PD   16-JAN-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 31
ID   ABU98048 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003017544-A1.
PD   23-JAN-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 32
ID   ABU91754 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003027277-A1.
PD   06-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 33
ID   ABU89447 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003036141-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 34
ID   ABU86288 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 35
ID   ABU67501 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003036162-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 36
ID   ABU80529 standard; protein; 335 AA.

DE Human PRO protein #96.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 37
ID ABU72515 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 38
ID ABU90898 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 39
ID ABO33957 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 40
ID ABR99447 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040063-A1.
PD 27-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 41
ID ABR98837 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040064-A1.
PD 27-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 42
ID ABO16360 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027267-A1.
PD 06-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 43
ID ABR92260 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036160-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 44
ID ABO18901 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044925-A1.
PD 06-MAR-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 45
ID ABR78322 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;

RESULT 46
ID ABU71974 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 47
ID ABU85058 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032114-A1.
PD 13-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 48
ID ABO00197 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032101-A1.
PD 13-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 49
ID ABO11529 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036124-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 50
ID ABO02174 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040054-A1.
PD 27-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 51
ID ABU88748 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036133-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 52
ID ABU83443 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036134-A1.
PD 20-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 53
ID ABO06244 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022294-A1.
PD 30-JAN-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 54
ID ABR59280 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027275-A1.
PD 06-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 55
ID ABO09342 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003027324-A1.
PD 06-FEB-2003.
    Query Match   100.0%;   Score 1772; DB 6; Length 335;
    Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 56
ID ABO19206 standard; protein; 335 AA.

DE   Novel human secreted and transmembrane protein PRO1138.
PN   US200303611B-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 57
ID   AB011224 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200303612B-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 58
ID   ABR66842 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200303614B-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 59
ID   AB016055 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200304006O-A1.
PD   27-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 60
ID   AB013761 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200304491G-A1.
PD   06-MAR-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 61
ID   ABU71528 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138
PN   US200301385S-A1.
PD   16-JAN-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 62
ID   AB065664 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein, SEQ ID 192.
PN   US200303615G-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 63
ID   AB007512 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US200303211J-A1.
PD   13-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 64
ID   AB003699 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200303612B-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 65
ID   ABR67147 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200302726G-A1.
PD   06-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 66
ID   AB015750 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.

PN   US200305448J-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 67
ID   ABU56031 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein, PRO1138.
PN   US200302229B-A1.
PD   30-JAN-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 68
ID   ABU72309 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US20021B263B-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 69
ID   ABU65359 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US200303210Z-A1.
PD   13-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 70
ID   ABU95304 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US200303611Z-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 71
ID   ABU71207 standard; protein; 335 AA.
DE   Human PRO1138 protein.
PN   US200303614J-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 72
ID   AB007817 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US200303213O-A1.
PD   13-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 73
ID   ABR70058 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200303213B-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 74
ID   ABR69391 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200303613Z-A1.
PD   20-FEB-2003.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 75
ID   AB001532 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US200300835J-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%;   Score 1772; DB 6;   Length 335;
      Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 76
ID   ABU81334 standard; protein; 335 AA.

DE Human PRO polypeptide #96.
PN US2003017542-A1.
PD 23-JAN-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 77
ID ABR60131 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032137-A1.
PD 13-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 78
ID ABU90982 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 79
ID ABR67866 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027269-A1.
PD 06-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 80
ID ABR65254 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027268-A1.
PD 06-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 81
ID ABR68476 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027274-A1.
PD 06-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 82
ID ABR71888 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027263-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 83
ID ABU59264 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2003027162-A1.
PD 06-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 84
ID ABU85368 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022295-A1.
PD 30-JAN-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 85
ID ABU89058 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003022297-A1.
PD 30-JAN-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 86
ID ABU83138 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003032105-A1.
PD 13-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 87
ID ABU94994 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032123-A1.
PD 13-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 88
ID ABU90542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032108-A1.
PD 13-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 89
ID ABU84053 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032111-A1.
PD 13-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 90
ID ABU93704 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 91
ID ABO25961 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 92
ID ABR64949 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027263-A1.
PD 06-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 93
ID ABO27303 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO138.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 94
ID ABR68781 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027271-A1.
PD 06-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 95
ID ABO06597 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036125-A1.
PD 20-FEB-2003.
   Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
   Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 96
ID ABR99142 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

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PN  US200304068-A1.
PD  27-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 97
ID  ABU57026 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003027280-A1.
PD  06-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 98
ID  ABU85978 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003022300-A1.
PD  30-JAN-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 99
ID  ABU82265 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003036136-A1.
PD  20-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 100
ID  ABU87276 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003036138-A1.
PD  20-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 101
ID  ABU83748 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003032109-A1.
PD  13-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 102
ID  ABU08122 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003040066-A1.
PD  27-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 103
ID  ABU92498 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003045684-A1.
PD  06-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 104
ID  ABU81833 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003032104-A1.
PD  13-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 105
ID  ABU65997 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003036157-A1.
PD  20-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 106
ID  ABU81168 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138.
PN  US2003027212-A1.
PD  06-FEB-2003.
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PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 107
ID  ABR59826 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003032120-A1.
PD  13-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 108
ID  ABU94014 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003036155-A1.
PD  20-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 109
ID  ABU99867 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003022296-A1.
PD  30-JAN-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 110
ID  ABR66537 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003027281-A1.
PD  06-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 111
ID  ABR90955 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003040058-A1.
PD  27-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 112
ID  ABO53283 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003027986-A1.
PD  06-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 113
ID  ABU58970 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein, #100.
PN  US2002142961-A1.
PD  03-OCT-2002.
PA  (GETH ) GENENTECH INC.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 114
ID  ABU94382 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003017540-A1.
PD  23-JAN-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 115
ID  ABU79264 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003032106-A1.
PD  13-FEB-2003.
    Query Match            100.0%;  Score 1772;  DB 6;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 116
ID  ABU85593 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003032129-A1.
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PD  13-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 117
ID  ABU86898  standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003032131-A1.
PD  13-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 118
ID  ABU94687  standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003032103-A1.
PD  13-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 119
ID  ABO04614  standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003032107-A1.
PD  13-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 120
ID  ABR70363  standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003032139-A1.
PD  13-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 121
ID  ABU92348  standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003022187-A1.
PD  30-JAN-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 122
ID  ABU98528  standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003022301-A1.
PD  30-JAN-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 123
ID  ABR65927  standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003036165-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 124
ID  ABR64644  standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003027262-A1.
PD  06-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 125
ID  ABU59413  standard; protein; 335 AA.
DE  Novel human secreted or transmembrane protein PRO1054.
PN  US2003027985-A1.
PD  06-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 126
ID  ABU79569  standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003032110-A1.
PD  13-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 127
ID  ABU92960  standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003036142-A1.
PD  20-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 128
ID  ABU95919  standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003036145-A1.
PD  20-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 129
ID  ABU91139  standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003036154-A1.
PD  20-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 130
ID  ABU90232  standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003036153-A1.
PD  20-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 131
ID  ABO09647  standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003044931-A1.
PD  06-MAR-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 132
ID  ABR58417  standard; protein; 335 AA.
DE  Human NOV27a.
PN  WO2003029423-A2.
PD  10-APR-2003.
PA  (CURA-) CURAGEN CORP.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 133
ID  ABO10919  standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003036150-A1.
PD  20-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 134
ID  ABR70973  standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003040069-A1.
PD  27-FEB-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 135
ID  ABU98285  standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003218493-A1.
PD  05-DEC-2002.
PA  (GETH ) GENENTECH INC.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 136
ID  ABU87581  standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003022293-A1.
PD  30-JAN-2003.
    Query Match          100.0%;   Score 1772;  DB 6;  Length 335;
    Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
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RESULT 137
ID   ABU91449 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003032128-A1.
PD   13-FEB-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 138
ID   ABU89290 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003036634-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 139
ID   ABU84663 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003032116-A1.
PD   13-FEB-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 140
ID   ABR69753 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003032122-A1.
PD   13-FEB-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 141
ID   ABU80130 standard; protein; 335 AA.
DE   Human PRO protein #96.
PN   US2003036139-A1.
PD   20-FEB-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 142
ID   ABU82497 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2002183494-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 143
ID   ABU92179 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003017476-A1.
PD   23-JAN-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 144
ID   ABU93399 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003017541-A1.
PD   23-JAN-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 145
ID   ABO09952 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003017543-A1.
PD   23-JAN-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 146
ID   ABO09037 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003036152-A1.
PD   20-FEB-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 147
ID   ABU96461 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003027993-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 148
ID   ABU10885 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2002123463-A1.
PD   05-SEP-2002.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 149
ID   ABU10605 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein #96.
PN   US2002127584-A1.
PD   12-SEP-2002.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 150
ID   ABU81637 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2002177164-A1.
PD   28-NOV-2002.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 151
ID   ABU72131 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003023042-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 152
ID   ABU95614 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003032115-A1.
PD   13-FEB-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 153
ID   ABU96823 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003032140-A1.
PD   13-FEB-2003.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 154
ID   ABR70668 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003040076-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 155
ID   ABO05019 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003008352-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
  Query Match   100.0%; Score 1772; DB 6; Length 335;
  Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 156
ID   ABO08427 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003044922-A1.

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PD  06-MAR-2003.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 157
ID  ABU88576 standard; protein; 335 AA.
DE  Human secreted and transmembrane polypeptide PRO1138.
PN  US2002197615-A1.
PD  26-DEC-2002.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 158
ID  ABO34090 standard; protein; 335 AA.
DE  Human PRO1138 polypeptide.
PN  US2003017981-A1.
PD  23-JAN-2003.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 159
ID  ABO05634 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003032118-A1.
PD  13-FEB-2003.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 160
ID  ABR74023 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003036135-A1.
PD  20-FEB-2003.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 161
ID  ABR95615 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003054455-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 162
ID  ABR80912 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003049741-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 163
ID  ABR81217 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003049743-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 164
ID  ABM00913 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003049769-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 165
ID  ABR88515 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003066743-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 166

ID  ABM77336 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003054479-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 167
ID  ABO28820 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003068685-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 168
ID  ABO31565 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003068725-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 169
ID  ABM07982 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003068752-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 170
ID  ABO40462 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003068682-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 171
ID  ABO35887 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003068701-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 172
ID  ABO44026 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003068755-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 173
ID  ADA77944 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003073180-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 174
ID  ABM24821 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003104539-A1.
PD  05-JUN-2003.
   Query Match         100.0%;  Score 1772;  DB 6;  Length 335;
   Best Local Similarity 100.0%;  Pred. No. 1.2e-162;
RESULT 175
ID  ABO03089 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
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PN  US2003036131-A1.
PD  20-FEB-2003.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 175
ID  ABR90345 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003040075-A1.
PD  27-FEB-2003.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 176
ID  ABM17259 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003054459-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 177
ID  ABR95005 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003044930-A1.
PD  06-MAR-2003.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 178
ID  ABR95310 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003040071-A1.
PD  27-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 179
ID  ADB17103 standard; protein; 335 AA.
DE  Human transmembrane PRO polypeptide (SeqID 46).
PN  US2003050462-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 180
ID  ABO21548 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003054471-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 181
ID  ABR97812 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003064452-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 182
ID  ABM77641 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003054473-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 183
ID  ABR87600 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003068705-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 184
ID  ABM27871 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003064440-A1.
PD  03-APR-2003.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 185
ID  ABM27871 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003064440-A1.
PD  03-APR-2003.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 186
ID  ABM06152 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003068704-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 187
ID  ABM03658 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003068722-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 188
ID  ABM35109 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003073183-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 189
ID  ABM26346 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003104549-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 190
ID  ABO48128 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003049749-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 191
ID  ABR92870 standard; protein; 335 AA.
DE  Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN  US2003064462-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 192
ID  ABO24631 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein (PRO) #96.
PN  US2003065159-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 193
ID  ADA37764 standard; protein; 335 AA.
DE  Human secreted/transmembrane protein PRO1138.
PN  US2003008297-A1.
PD  09-JAN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match             100.0%;  Score 1772; DB 6;  Length 335;
    Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 194
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ID   ABM11642 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 195
ID   ABM02743 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 196
ID   ABM16039 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 197
ID   ABO27600 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003064451-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 198
ID   ABM07067 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068699-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 199
ID   ABM21161 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 200
ID   ABM09507 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003071175-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 201
ID   ABO41377 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 202
ID   ABO36192 standard; protein; 335 AA.

DE   Human PRO polypeptide #96.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 204
ID   ABO43721 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 205
ID   ABM76421 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003082717-A1.
PD   01-MAY-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 206
ID   ABM76117 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 207
ID   ABM25736 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104542-A1.
PD   05-JUN-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 208
ID   ABM26041 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104543-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 209
ID   ADA21450 standard; protein; 335 AA.
DE   Human secreted/transmembrane polypeptide PRO1138.
PN   US2003054404-A1.
PD   20-MAR-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 210
ID   ABO03394 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003036127-A1.
PD   20-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 211
ID   ABO02479 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003040061-A1.
PD   27-FEB-2003.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 212
ID   ABO44261 standard; protein; 335 AA.
DE   Human secreted/transmembrane polypeptide PRO 1138.
PN   US2003018172-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 6; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 213

ID ABR90650 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036130-A1.
PD 20-FEB-2003.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 214
ID ABR73718 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 215
ID ABO16970 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 216
ID ABR94395 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 217
ID ABR75902 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 218
ID ABR71278 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 219
ID ABR93175 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 220
ID ADA10237 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 221
ID ABR93480 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 222
ID ABR87905 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 223
ID ABO27905 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 224
ID ABO30040 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 225
ID ABO33249 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 226
ID ABM04937 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 227
ID ABM08897 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 228
ID ABO36497 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 229
ID ABO35582 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 230
ID ABO39547 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;
   Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 231
ID ABM10422 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
   Query Match   100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 232
ID   ABM11947 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104555-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 233
ID   ABO52093 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049768-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 234
ID   ABO52398 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049771-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 235
ID   ABO23716 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003032134-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 236
ID   ADA19908 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003069394-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 237
ID   ADB17291 standard; protein; 335 AA.
DE   Human transmembrane PRO polypeptide (SeqID 46).
PN   US2003050465-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 238
ID   ADA17781 standard; protein; 335 AA.
DE   Human PRO1138 polypeptide.
PN   US2003054987-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 239
ID   ABR97202 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054481-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 240
ID   ABR86990 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049778-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 241
ID   ABM11032 standard; protein; 335 AA.

DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049782-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 242
ID   ABM28176 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054476-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 243
ID   ABO32175 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 244
ID   ABM15302 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 245
ID   ABM06457 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 246
ID   ABM04268 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 247
ID   ABM22381 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 248
ID   ABM07677 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 249
ID   ABO40767 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 250
ID   ABM35414 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.

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PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 251
ID   ABM33177 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003087374-A1.
PD   08-MAY-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 252
ID   AB052703 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 253
ID   AB050263 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 254
ID   ABU99257 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003040055-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 255
ID   AB004309 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003040074-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 256
ID   AB005939 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 257
ID   ABM18479 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 258
ID   ADA27889 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003054359-A1.
PD   20-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 259
ID   ABR97507 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 260
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ID   ABR80607 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 261
ID   ABM01218 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 262
ID   ABR88820 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073169-A1.
PD   17-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 263
ID   ABM13472 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 264
ID   ABM20856 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 265
ID   AB041987 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049745-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 266
ID   AB042597 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 267
ID   ABM10117 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 268
ID   AB038632 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003066773-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 269
ID   ABM32872 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
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PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 270
ID   ABM22686 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073373-A1.
PD   08-MAY-2003.
RESULT 271
ID   ABM74897 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003096353-A1.
PD   22-MAY-2003.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 272
ID   ADA79736 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003073173-A1.
PD   17-APR-2003.
RESULT 273
ID   ABR96287 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054458-A1.
PD   20-MAR-2003.
RESULT 274
ID   ABM02438 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003059886-A1.
PD   27-MAR-2003.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 275
ID   ABR86380 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049758-A1.
PD   13-MAR-2003.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 276
ID   ABR86685 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
RESULT 277
ID   ABM16649 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 278
ID   ABM29701 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;

RESULT 279
ID   ABO29125 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 280
ID   ABM23906 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 281
ID   ABM23296 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068753-A1.
PD   10-APR-2003.
RESULT 282
ID   ABM22076 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 283
ID   ABO37717 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 284
ID   ABM28481 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003082715-A1.
PD   01-MAY-2003.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 285
ID   ABM28786 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003082716-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 286
ID   ABM66430 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 287
ID   ABM75812 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match              100.0%;   Score 1772;   DB 6;   Length 335;
     Best Local Similarity    100.0%;   Pred. No. 1.2e-162;
RESULT 288
ID   ABM34092 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
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PN   US200309359-A1
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 289
ID   ABM34397 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200310061-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 290
ID   ABO20328 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200303125-A1.
PD   13-FEB-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 291
ID   ABO21243 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200305454-A1.
PD   20-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 292
ID   ABO22158 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200305477-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 293
ID   ADA20080 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US200305222-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 294
ID   ABO34189 standard; protein; 335 AA.
DE   Human secreted/transmembrane polypeptide PRO 1138.
PN   US200306601-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 295
ID   ABR96592 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200305832-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 296
ID   ADA94469 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US200305832-A1.
PD   27-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 297
ID   ABR85770 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200304953-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;

     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 298
ID   ABR99752 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200304963-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 299
ID   ABM00608 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200307172-A1.
PD   17-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 300
ID   ABM00303 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200307172-A1.
PD   17-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 301
ID   ABO29735 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200306870-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 302
ID   ABM23601 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200306873-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 303
ID   ABM29396 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200306679-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 304
ID   ABO38327 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US200306767-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 305
ID   ABO45627 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US200307182-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 306
ID   ABM20551 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US200310455-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 307
ID   ADA81463 standard; protein; 335 AA.
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DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003092121-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 308
ID   ABO16665 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003027275-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 309
ID   ABO18291 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003044920-A1.
PD   06-MAR-2003.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 310
ID   ABO22718 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003027265-A1.
PD   06-FEB-2003.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 311
ID   ABO23023 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003054461-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 312
ID   ABR92565 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064446-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 313
ID   ABR81522 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 314
ID   ABM77946 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049783-A1.
PD   13-MAR-2003.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 315
ID   ABR89735 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073171-A1.
PD   17-APR-2003.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 316
ID   ABM26651 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003032121-A1.
PD   13-FEB-2003.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;

RESULT 317
ID   ABM13777 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064458-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 318
ID   ABO28515 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003064460-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 319
ID   ABO30345 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003064464-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 320
ID   ABM07372 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068702-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 321
ID   ABM03963 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068734-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 322
ID   ABO37107 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068719-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 323
ID   ABO41682 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068729-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 324
ID   ABO35277 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003068738-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 325
ID   ABM25126 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104540-A1.
PD   05-JUN-2003.
     Query Match
     Best Local Similarity 100.0%;   Score 1772; DB 6;   Length 335;
                            100.0%;   Pred. No. 1.2e-162;
RESULT 326
ID   ABO47518 standard; protein; 335 AA.

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DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049742-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 327
ID   ABO47823 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049747-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 328
ID   ABO48433 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049750-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 329
ID   ABO51483 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049766-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 330
ID   ABO51788 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049767-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 331
ID   ABO50568 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049779-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 332
ID   ABR79692 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003040059-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 333
ID   ABM16954 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003040078-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 334
ID   ABO17986 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003044918-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 335
ID   ABO20938 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003032132-A1.
PD   13-FEB-2003.


     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 336
ID   ABR96697 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054462-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 337
ID   ADA38694 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003059780-A1.
PD   27-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 338
ID   ABM12252 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064445-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 339
ID   ABM16344 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064449-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 340
ID   ABM24211 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064441-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 341
ID   ABM14692 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068696-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 342
ID   ABM04573 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068712-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 343
ID   ABM06762 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068730-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 344
ID   ABM09202 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073174-A1.
PD   17-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 6;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 345
ID   ABO39242 standard; protein; 335 AA.
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DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068775-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 347
ID   ABM25431 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104541-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 348
ID   ABM19941 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104554-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 349
ID   ABO46847 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049762-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 350
ID   ABO47152 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049765-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 351
ID   ADA83261 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 352
ID   ABR71583 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003032133-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 353
ID   ABR72193 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003032136-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Best Local Similarity   100.0%;   Score 1772;  DB 6;  Length 335;
  Query Match             100.0%;   Pred. No. 1.2e-162;
RESULT 354
ID   ABR95532 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003036129-A1.
PD   20-FEB-2003.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 355
ID   ABO06902 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003040053-A1.
PD   27-FEB-2003.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 356
ID   ABR84855 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003040057-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 357
ID   ABR73413 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054467-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 358
ID   ABR76507 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003044932-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 359
ID   ABR73108 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003027270-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 360
ID   ABM18174 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003054469-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 361
ID   ABO20633 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003032126-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 362
ID   ABO25376 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003054463-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 363
ID   ABO25681 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003054466-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;   Score 1772;  DB 6;  Length 335;
  Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 364
ID   ABR94090 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003059879-A1.
PD   27-MAR-2003.
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PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 365
ID   ADA92815 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003060407-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 366
ID   ABR79997 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049738-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 367
ID   ABM11337 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064469-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 368
ID   ABO32944 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003064453-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 369
ID   ABO30650 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003064468-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 370
ID   ABO30955 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003064466-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 371
ID   ABM27261 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068769-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 372
ID   ABM30006 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003045700-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 373
ID   ABM05542 standard; protein; 335 AA.

RESULT 374
ID   ABM15607 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068698-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 375
ID   ABM08592 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068759-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 376
ID   ABO42292 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049748-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 377
ID   ABO38022 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068765-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 378
ID   ABO45932 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049754-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 379
ID   ABM66735 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068688-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 380
ID   ADB20304 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003082767-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 381
ID   ABM19636 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104552-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 382
ID   ABO49348 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049774-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1772; DB 6;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 383
ID   ABO49653 standard; protein; 335 AA.

DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049775-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity   100.0%;   Score 1772;   DB 6;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 384
ID   ADA78556 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003073181-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 6;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 385
ID   ABR88210 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068720-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 6;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 386
ID   ADA00377 standard; protein; 335 AA.
DE   Human secreted/transmembrane polypeptide PRO 138.
PN   US2003027992-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 6;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 387
ID   ABM26956 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068739-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 6;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 388
ID   ABM03353 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068763-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 6;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 389
ID   ABO39852 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068609-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 6;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 390
ID   ABO49958 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049776-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 391
ID   ABO50873 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049780-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 392
ID   ABO05329 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.

PN   US2003036126-A1.
PD   20-FEB-2003.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 393
ID   ABR74613 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003044924-A1.
PD   06-MAR-2003.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 394
ID   ABR77112 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003044927-A1.
PD   06-MAR-2003.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 395
ID   ABM17869 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003040072-A1.
PD   27-FEB-2003.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 396
ID   ABR95920 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003040073-A1.
PD   27-FEB-2003.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 397
ID   ABO21853 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003054475-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 398
ID   ABO20023 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003032124-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 399
ID   ABO24326 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003064467-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 400
ID   ABR86075 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049759-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 401
ID   ABM10727 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064455-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
                               100.0%;   Pred. No. 1.2e-162;
RESULT 402
ID   ABM76726 standard; protein; 335 AA.

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DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054465-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 403
ID   ABR89430 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073170-A1.
PD   17-APR-2003.
RESULT 404
ID   ABM12557 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073176-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 405
ID   ABM05847 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068717-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 406
ID   ABO34972 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 407
ID   ABM03048 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 408
ID   ABM19026 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 409
ID   ABM19331 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 410
ID   ABO46542 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 411
ID   ABO49043 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049757-A1.

PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 412
ID   ABR69086 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003022273-A1.
PD   06-FEB-2003.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 413
ID   ABR89125 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003036119-A1.
PD   20-FEB-2003.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 414
ID   ABR72498 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003036120-A1.
PD   20-FEB-2003.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 415
ID   ABR74328 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 416
ID   ABO18596 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003044921-A1.
PD   06-MAR-2003.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 417
ID   ABR80302 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 418
ID   ABM01523 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 419
ID   ABM02133 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 420
ID   ABR87295 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;     Score 1772;  DB 7;   Length 335;
  Best Local Similarity   100.0%;     Pred. No. 1.2e-162;
RESULT 421
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ID    ABM12862 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003073186-A1.
PD    17-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 422
ID    ABM30616 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003064443-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 423
ID    ABM24516 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003064444-A1.
PD    03-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 424
ID    ABO29430 standard; protein; 335 AA.
DE    Human secreted/transmembrane protein (PRO) #96.
PN    US2003068697-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 425
ID    ABO31260 standard; protein; 335 AA.
DE    Human secreted/transmembrane protein (PRO) #96.
PN    US2003068710-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 426
ID    ABM14387 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003068686-A1.
PD    10-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 427
ID    ABM09812 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003073178-A1.
PD    17-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 428
ID    ABO38937 standard; protein; 335 AA.
DE    Human secreted/transmembrane protein (PRO) #96.
PN    US2003068774-A1.
PD    17-APR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 429
ID    ABM34702 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003104538-A1.
PD    05-JUN-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 430
ID    ABO51178 standard; protein; 335 AA.
DE    Human secreted/transmembrane protein (PRO) #96.

PN    US2003049781-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 431
ID    ABO04004 standard; protein; 335 AA.
DE    Human secreted/transmembrane protein (PRO) #96.
PN    US2003036158-A1.
PD    20-FEB-2003.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 432
ID    ABO10474 standard; protein; 335 AA.
DE    Human PRO polypeptide #96.
PN    US2003036151-A1.
PD    20-FEB-2003.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 433
ID    ABO53176 standard; protein; 335 AA.
DE    Human secreted/transmembrane protein PRO1138.
PN    US2003044806-A1.
PD    06-MAR-2003.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 434
ID    ABR77717 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003040067-A1.
PD    27-FEB-2003.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 435
ID    ABR78927 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003054456-A1.
PD    20-MAR-2003.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 436
ID    ABO24021 standard; protein; 335 AA.
DE    Human secreted/transmembrane protein (PRO) #96.
PN    US2003054482-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 437
ID    ABR93785 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003054457-A1.
PD    20-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 438
ID    ABM01828 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003059883-A1.
PD    27-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 439
ID    ABM78251 standard; protein; 335 AA.
DE    Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN    US2003049764-A1.
PD    13-MAR-2003.
PA    (GETH ) GENENTECH INC.
      Query Match             100.0%;  Score 1772; DB 7; Length 335;
      Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 440
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ID   ABR90040 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 441
ID   ADA22376 standard; protein; 335 AA.
DE   Human secreted/transmembrane polypeptide PRO1138
PN   US2003040473-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 442
ID   ABM27566 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064442-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 443
ID   ABM13167 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003064450-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 444
ID   AB031870 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068731-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 445
ID   ABM14082 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068683-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 446
ID   ABM08287 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068754-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 447
ID   AB040157 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068681-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 448
ID   ABM74592 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003096351-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 449
ID   ABM33787 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003096358-A1.
PD   22-MAY-2003.

PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 450
ID   ABM20246 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104456-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 451
ID   AB048738 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049756-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 452
ID   AB022546 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003017982-A1.
PD   23-JAN-2003.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 453
ID   ABR72803 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003036122-A1.
PD   20-FEB-2003.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 454
ID   AB015445 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003036121-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 455
ID   ABR85160 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003040065-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 456
ID   AB015140 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003044919-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 457
ID   AB017275 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003040077-A1.
PD   27-FEB-2003.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 458
ID   ABM17564 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003044928-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;   Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;
RESULT 459
ID   ADA06542 standard; protein; 335 AA.
DE   Human secreted/transmembrane PRO polypeptide #71.
PN   US2003049638-A1.
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PD   13-MAR-2003.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 460
ID   ADA39235 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003059782-A1.
PD   27-MAR-2003.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 461
ID   ABR85465 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003049746-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
RESULT 462
ID   ABM77031 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003054464-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 463
ID   ABO28210 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003064459-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 464
ID   ABM22991 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068757-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 465
ID   ABM30311 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068723-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 466
ID   ABM21771 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068741-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 467
ID   ABM21466 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068744-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 468
ID   ABM14997 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068766-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;

Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 469
ID   ABO41072 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068694-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 470
ID   ABO36802 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068715-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 471
ID   ABO37412 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003068726-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 472
ID   ABM75202 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003104544-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 473
ID   ABM33482 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003096357-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 474
ID   ABO46237 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2003049760-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 475
ID   ABO82627 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003049755-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 476
ID   ADB85619 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003049735-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 477
ID   ADB96261 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003054403-A1.
PD   20-MAR-2003.
Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 478

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ID   ABM31836 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068680-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 479
ID   ABM31226 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068762-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 480
ID   ADB85935 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003054472-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 481
ID   ABM32141 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068708-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 482
ID   ABM32446 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068713-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 483
ID   ADB68298 standard; protein; 335 AA.
DE   Human PRO1138 protein.
PN   US2003065161-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 484
ID   ADB68105 standard; protein; 335 AA.
DE   Human PRO1138 protein.
PN   US2003066600-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 485
ID   ABM31531 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068761-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 486
ID   ABM30921 standard; protein; 335 AA.
DE   Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN   US2003068771-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 487
ID   ADB90922 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003083473-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 488
ID   ADC57733 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003027754-A1.
PD   06-FEB-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 489
ID   ADC55097 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003045463-A1.
PD   06-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 490
ID   ADC11964 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003049681-A1.
PD   13-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 491
ID   ADC07002 standard; protein; 335 AA.
DE   Human PRO1138 protein.
PN   US2003060602-A1.
PD   27-MAR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 492
ID   ADC56386 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003064375-A1.
PD   03-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 493
ID   ADC17181 standard; protein; 335 AA.
DE   Mammalian PRO polypeptide (SeqID 46).
PN   US2003065143-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 494
ID   ADC07441 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003066647-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 495
ID   ADC11431 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003069403-A1.
PD   10-APR-2003.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 496
ID   ADC14879 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003073208-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;  Score 1772;  DB 7;  Length 335;
     Best Local Similarity   100.0%;  Pred. No. 1.2e-162;

RESULT 497
ID   ADC52374 standard; protein; 335 AA.
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DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003118882-A1.
PD   24-JUL-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity   100.0%;   Score 1772;   DB 7;   Length 335;
     Query Match   100.0%;   Pred. No. 1.2e-162.
RESULT 498
ID   ADC14553 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003082546-A1.
PD   01-MAY-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 499
ID   ADD08085 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003068623-A1.
PD   10-APR-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 500
ID   ADC81910 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003083461-A1.
PD   01-MAY-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 501
ID   ADD07552 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 502
ID   ADC82443 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003059833-A1.
PD   27-MAR-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 503
ID   ADD05665 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 504
ID   ADD08623 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003073090-A1.
PD   17-APR-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 505
ID   ADD06872 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 506
ID   ADC89503 standard; protein; 335 AA.
DE   Human natural killer cell surface receptor CS1.
PN   US2003113332-A1.
PD   19-JUN-2003.
PA   (UYNT-) UNIV NORTH TEXAS HEALTH SCI CENT.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.

RESULT 507
ID   ADC83119 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003059783-A1.
PD   27-MAR-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 508
ID   ADD67525 standard; protein; 335 AA.
DE   Human Ly1728P protein SEQ ID NO:2.
PN   WO2003062401-A2.
PD   31-JUL-2003.
PA   (CORI-) CORIXA CORP.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 509
ID   ADD55226 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003077593-A1.
PD   24-APR-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 510
ID   ADD36050 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003105298-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 511
ID   ADD56184 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2003077594-A1.
PD   24-APR-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 512
ID   ADD54622 standard; protein; 335 AA.
DE   Human PRO polypeptide #71.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 513
ID   ADE26776 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003087304-A1.
PD   08-MAY-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 514
ID   ADE26243 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003087305-A1.
PD   08-MAY-2003.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 515
ID   ADF67180 standard; protein; 335 AA.
DE   Human PRO1138 amino acid sequence SEQ ID NO:253.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162.
RESULT 516
ID   ADG01051 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003078387-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.

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      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 517
ID  ADG08604 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180793-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 518
ID  ADG02660 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003207397-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 519
ID  ADG01367 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003207399-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 520
ID  ADF95542 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003207398-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 521
ID  ADF95225 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180795-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 522
ID  ADG12357 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003207392-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 523
ID  ADH24078 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180918-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 524
ID  ADH34104 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180858-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 525
ID  ADH29937 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180859-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;

RESULT 526
ID  ADH23908 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180919-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 527
ID  ADH09017 standard; protein; 335 AA.
DE  Human PRO polypeptide #96.
PN  US2003207395-A1.
PD  06-NOV-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 528
ID  ADG85312 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180904-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 529
ID  ADH24588 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180907-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 530
ID  ADH37444 standard; protein; 335 AA.
DE  Human secreted and transmembrane protein PRO138 cDNA.
PN  US2003181646-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 531
ID  ADH02033 standard; protein; 335 AA.
DE  Human PRO polypeptide #23.
PN  US2003180837-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 532
ID  ADH37614 standard; protein; 335 AA.
DE  Human secreted and transmembrane protein PRO138 cDNA.
PN  US2003181648-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 533
ID  ADG85652 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180905-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 534
ID  ADH24248 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180914-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
      Query Match           100.0%      Score 1772;  DB 7;  Length 335;
      Best Local Similarity 100.0%      Pred. No. 1.2e-162;
RESULT 535
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ID  ADH38542 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181643-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 536
ID  ADG83663 standard; protein; 335 AA.
DE  Human PRO polypeptide #23.
PN  US2003180794-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 537
ID  ADH29471 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180860-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 538
ID  ADH27587 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003180906-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 539
ID  ADH37784 standard; protein; 335 AA.
DE  Human secreted and transmembrane protein PRO1138 cDNA.
PN  US2003181647-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 540
ID  ADH37961 standard; protein; 335 AA.
DE  Human secreted and transmembrane protein PRO1138 cDNA.
PN  US2003180920-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 541
ID  ADH57381 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181636-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 542
ID  ADH53523 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181641-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 543
ID  ADH53693 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181641-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 544
ID  ADH52029 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181638-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 545
ID  ADH49884 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181639-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 546
ID  ADI25394 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181696-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 547
ID  ADH90187 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181698-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 548
ID  ADI25564 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181669-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 549
ID  ADH97738 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181672-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 550
ID  ADI35434 standard; protein; 335 AA.
DE  Human PRO polypeptide #71.
PN  US2003050457-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 551
ID  ADI11943 standard; protein; 335 AA.
DE  Human PRO polypeptide #23.
PN  US2003181686-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 552
ID  ADI03586 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181656-A1.
PD  25-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        100.0%;  Score 1772;  DB 7;  Length 335;
    Best Local Similarity  100.0%;  Pred. No. 1.2e-162;
RESULT 553
ID  ADH90017 standard; protein; 335 AA.
DE  Novel human secreted and transmembrane protein PRO1138.
PN  US2003181697-A1.
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PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 554
ID   ADH99926 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003049682-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 555
ID   ADH98418 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181707-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 556
ID   ADI11093 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181682-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 557
ID   ADI11603 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181684-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 558
ID   ADH98248 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181709-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 559
ID   ADH98588 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181708-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 560
ID   ADH98078 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180848-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 561
ID   ADI05066 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181673-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
      Best Local Similarity 100.0%;
Query Match   100.0%; Score 1772; DB 7; Length 335;
RESULT 562
ID   ADI03416 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO138.
PN   US2003181654-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.

Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 563
ID   ADI04811 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181657-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 564
ID   ADH78265 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181668-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 565
ID   ADI19609 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181676-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 566
ID   ADH90357 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181699-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 567
ID   ADI01076 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181653-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 568
ID   ADH77925 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181666-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 569
ID   ADH97908 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181674-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 570
ID   ADI01293 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003190669-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;
      Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 571
ID   ADI01988 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181652-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   100.0%; Score 1772; DB 7; Length 335;

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     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 572
ID   ADI03246 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181655-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 573
ID   ADI11433 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181681-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 574
ID   ADI02335 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181650-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 575
ID   ADI11773 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181685-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 576
ID   ADI05410 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003190716-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 577
ID   ADH79482 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003191290-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 578
ID   ADI19439 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181675-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 579
ID   ADI05240 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181677-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 580
ID   ADH79652 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003191288-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;

RESULT 581
ID   ADI01478 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181678-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 582
ID   ADI01648 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181679-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 583
ID   ADI01818 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181680-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 584
ID   ADH79822 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003191289-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 585
ID   ADI04640 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003171550-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 586
ID   ADI02776 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181651-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 587
ID   ADH78095 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181667-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 588
ID   ADI25734 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181670-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 589
ID   ADI25904 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181671-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772;   DB 7;   Length 335;
     Best Local Similarity 100.0%;   Pred. No. 1.2e-162;
RESULT 590
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ID   ADK65416 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003073821-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 7; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 591
ID   ADH98758 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003191284-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 7; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 592
ID   ADH79999 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003191287-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 7; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 593
ID   ADL32798 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003207396-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 7; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 594
ID   ADM30132 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003073813-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 7; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 595
ID   ADL93730 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003040013-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 7; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 596
ID   ADC52184 standard; protein; 335 AA.
DE   Novel human secreted/transmembrane protein (PRO) #96.
PN   US2003130483-A1.
PD   10-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 597
ID   ADE74329 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003211572-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 598
ID   ADE74941 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein (PRO) #96.
PN   US2003211574-A1.
PD   13-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 599
ID   ADF35379 standard; protein; 335 AA.
DE   Human PRO1138 polypeptide.
PN   US2003194760-A1.

PD   16-OCT-2003.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 600
ID   ADG11629 standard; protein; 335 AA.
DE   Human PRO1138 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 601
ID   ADF96154 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003215909-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 602
ID   ADG04425 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003215912-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 603
ID   ADG00585 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003215911-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 604
ID   ADH06616 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180852-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 605
ID   ADH06446 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180853-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 606
ID   ADG68867 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180855-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 607
ID   ADH27757 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180912-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 608
ID   ADH25098 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180913-A1.
PD   25-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             100.0%;   Score 1772; DB 8; Length 335;
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Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 609
ID ADH33730 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 610
ID ADG82841 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 611
ID ADH02373 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 612
ID ADH07980 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 613
ID ADG69377 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 614
ID ADH39198 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 615
ID ADH26122 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 616
ID ADG83938 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 617
ID ADH19499 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%;

RESULT 618
ID ADG85482 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 619
ID ADH06276 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 620
ID ADH30106 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 621
ID ADH24418 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 622
ID ADH33091 standard; protein; 335 AA.
DE Human PRO polyeptide #96.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 623
ID ADG69547 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 624
ID ADH07810 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 625
ID ADG85822 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 626
ID ADH39368 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e-162;
RESULT 627

ID   ADH33560 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181637-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 628
ID   ADH33900 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181644-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 629
ID   ADH01110 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003180838-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 630
ID   ADG69717 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180843-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 631
ID   ADH20992 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003224358-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 632
ID   ADH02203 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003180841-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 633
ID   ADG69207 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180847-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 634
ID   ADG85992 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180862-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 635
ID   ADH24928 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180909-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
RESULT 636
ID   ADH39545 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.

PN   US2003180915-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 637
ID   ADH20032 standard; protein; 335 AA.
DE   Human secreted/transmembrane protein PRO1138.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 638
ID   ADH02543 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003180840-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 639
ID   ADG69037 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180849-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 640
ID   ADH07640 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180850-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 641
ID   ADG86162 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180863-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 642
ID   ADH24758 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180908-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 643
ID   ADH25806 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180911-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 644
ID   ADH38372 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180922-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Best Local Similarity 100.0%;
     Query Match 100.0%;   Score 1772; DB 8; Length 335;
                           Pred. No. 1.2e-162;
RESULT 645
ID   ADH57211 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181642-A1.

PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 646
ID   ADH52199 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180921-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 647
ID   ADH49565 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003180857-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 648
ID   ADH90527 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181700-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 649
ID   ADI11263 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003181683-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 650
ID   ADH98928 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003190698-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 651
ID   ADI02158 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003190699-A1.
PD   09-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 652
ID   ADH90697 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181701-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 653
ID   ADJ54830 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2004023321-A1.
PD   05-FEB-2004.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 654
ID   ADJ98572 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003187197-A1.
PD   02-OCT-2003.

PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 655
ID   ADJ98742 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003187228-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 656
ID   ADH78901 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181703-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 657
ID   ADJ99135 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003186408-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 658
ID   ADJ99305 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003187196-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 659
ID   ADJ98923 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003187242-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 660
ID   ADH79071 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003181702-A1.
PD   25-SEP-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 661
ID   ADK00931 standard; protein; 335 AA.
DE   Human PRO polypeptide #23.
PN   US2003186407-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 662
ID   ADK14452 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2003187229-A1.
PD   02-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   100.0%; Score 1772; DB 8; Length 335;
     Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 663
ID   ADJ64601 standard; protein; 335 AA.
DE   Human PRO polypeptide #96.
PN   US2004038337-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 8;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 664
ID ADM31497 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 8;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 665
ID ADM36544 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 8;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 666
ID ADM40349 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 8;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 667
ID ADM80901 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 8;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 668
ID ADN37957 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 8;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 669
ID ADU87689 standard; protein; 335 AA.
DE Human CS1 (SLAMF7) protein.
PN WO2004100898-A2.
PD 25-NOV-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match   100.0%;   Score 1772; DB 8;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 670
ID ADY19131 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO 4937.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 9;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 671
ID ADY77741 standard; protein; 335 AA.
DE Neoplastic disease detection protein PRO1138.
PN US2005059102-A1.
PD 17-MAR-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W I.

Query Match   100.0%;   Score 1772; DB 9;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 672
ID AEA38506 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #139.
PN US2005112725-A1.
PD 26-MAY-2005.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 9;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 673
ID AED50187 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2005163766-A1.
PD 28-JUL-2005.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 9;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 674
ID AED97202 standard; protein; 335 AA.
DE Human CS1 polypeptide #1.
PN WO2005102387-A2.
PD 03-NOV-2005.
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match   100.0%;   Score 1772; DB 9;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 675
ID AEF12572 standard; protein; 335 AA.
DE Human PRO1138 protein SEQ ID NO:46.
PN US2006008901-A1.
PD 12-JAN-2006.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 10;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 676
ID AEF74261 standard; protein; 335 AA.
DE Human PRO1138 protein SEQ ID NO:46.
PN US2005260647-A1.
PD 24-NOV-2005.
PA (EATO/) EATON D L.
PA (FILV/) FILVAROFF E.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI J C.
PA (GURN/) GURNEY A L.
PA (WATA/) WATANABE C K.
PA (WOOD/) WOOD W L.

Query Match   100.0%;   Score 1772; DB 10;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 677
ID AEG62879 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2006073544-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 10;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 678
ID AEG72702 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2006074226-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 10;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 679
ID AEG62267 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2006073545-A1.
PD 06-APR-2006.
PA (GETH) GENENTECH INC.

Query Match   100.0%;   Score 1772; DB 10;   Length 335;
Best Local Similarity   100.0%;   Pred. No. 1.2e-162;
RESULT 680

ID   AEG88184 standard; protein; 335 AA.
DE   Human PRO protein amino acid sequence - SEQ ID 192.
PN   US2006074227-A1.
PD   06-APR-2006.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%; Score 1772; DB 10; Length 335;
      Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 681
ID   AEH17500 standard; protein; 335 AA.
DE   Human tumor overexpressed cDNA protein product PRO1138 SEQ ID NO: 192.
PN   US2006094864-A1.
PD   04-MAY-2006.
PA   (GETH) GENENTECH INC.
      Query Match   100.0%; Score 1772; DB 10; Length 335;
      Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 682
ID   AEH43599 standard; protein; 335 AA.
DE   PRO1138 protein sequence, SEQ ID 46.
PN   US2006099657-A1.
PD   11-MAY-2006.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
      Query Match   100.0%; Score 1772; DB 10; Length 335;
      Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 683
ID   AEJ11924 standard; protein; 335 AA.
DE   Novel human secreted and transmembrane protein PRO1138.
PN   US2006160186-A1.
PD   20-JUL-2006.
PA   (EATO/) EATON D L.
PA   (FILV/) FILVAROFF E.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
      Query Match   100.0%; Score 1772; DB 10; Length 335;
      Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 684
ID   AAB32373 standard; protein; 336 AA.
DE   Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.
PN   WO200047602-A1.
PD   17-AUG-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
      Query Match   100.0%; Score 1772; DB 3; Length 336;
      Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 685
ID   ADS98579 standard; protein; 340 AA.
DE   Protein factor discovery related human contig polypeptide, SEQ ID 843.
PN   WO200408874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
      Query Match   100.0%; Score 1772; DB 8; Length 340;
      Best Local Similarity   100.0%; Pred. No. 1.2e-162;
RESULT 686
ID   ADD18672 standard; protein; 335 AA.
DE   Human disease related protein SeqID103.
PN   WO200301862-1-A2.
PD   06-MAR-2003.
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
      Query Match   99.8%; Score 1769; DB 7; Length 335;
      Best Local Similarity   99.7%; Pred. No. 2.3e-162;
RESULT 687

ID   ADJ69599 standard; protein; 335 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1405.
PN   WO200308768-A2.
PD   23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
      Query Match   99.8%; Score 1769; DB 7; Length 335;
      Best Local Similarity   99.7%; Pred. No. 2.3e-162;
RESULT 688
ID   ABR58418 standard; protein; 348 AA.
DE   Human NOV27b.
PN   WO200302423-A2.
PD   10-APR-2003.
PA   (CURA-) CURAGEN CORP.
      Query Match   99.1%; Score 1755.5; DB 6; Length 348;
      Best Local Similarity   96.3%; Pred. No. 5e-161;
RESULT 689
ID   AD070729 standard; protein; 348 AA.
DE   Human novel protein NOV27b.
PN   US20040388-77-A1.
PD   26-FEB-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CATT/) CATTERTON E.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUOX/) GUO X.
PA   (JIWW/) JI W.
PA   (KEKU/) KEKUDA R.
PA   (LEAC/) LEACH M D.
PA   (LILL/) LI L.
PA   (MILL/) MILLER C E.
PA   (PATT/) PATTURAJAN M.
PA   (RIEG/) RIEGER D K.
PA   (ROTH/) ROTHENBERG M E.
PA   (SHIM/) SHIMKETS R A.
PA   (SMIT/) SMITHSON G.
PA   (SPYT/) SPYTEK K A.
PA   (TAUP/) TAUPIER R J.
PA   (VERN/) VERNET C A M.
PA   (VOSS/) VOSS E Z.
PA   (ZERH/) ZERHUSEN B D.
PA   (ZHON/) ZHONG M.
      Query Match   99.1%; Score 1755.5; DB 8; Length 348;
      Best Local Similarity   96.3%; Pred. No. 5e-161;
RESULT 690
ID   AD070727 standard; protein; 336 AA.
DE   Human novel protein NOV27a.
PN   US20040388-77-A1.
PD   26-FEB-2004.
PA   (ALSO/) ALSOBROOK J P.
PA   (ANDE/) ANDERSON D W.
PA   (BOLD/) BOLDOG F L.
PA   (BURG/) BURGESS C E.
PA   (CATT/) CATTERTON E.
PA   (EDIN/) EDINGER S R.
PA   (ELLE/) ELLERMAN K.
PA   (GERL/) GERLACH V.
PA   (GORM/) GORMAN L.
PA   (GUOX/) GUO X.
PA   (JIWW/) JI W.
PA   (KEKU/) KEKUDA R.
PA   (LEAC/) LEACH M D.
PA   (LILL/) LI L.
PA   (MILL/) MILLER C E.
PA   (PATT/) PATTURAJAN M.
PA   (RIEG/) RIEGER D K.
PA   (ROTH/) ROTHENBERG M E.
PA   (SHIM/) SHIMKETS R A.

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PA   (SMIT/)  SMITHSON G.
PA   (SPYT/)  SPYTEK K A.
PA   (TAUP/)  TAUPIER R J.
PA   (VERN/)  VERNET C A M.
PA   (VOSS/)  VOSS E Z.
PA   (ZERH/)  ZERHUSEN B D.
PA   (ZHON/)  ZHONG M.
     Query Match           97.6%;  Score 1729.5;  DB 8;  Length 336;
     Best Local Similarity  98.5%;  Pred. No. 1.6e-158;
RESULT 691
ID   AAY44610 standard; protein; 312 AA.
DE   Mature human myocardium protein-7.
PN   WO9967387-A2.
PD   29-DEC-1999.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match           93.3%;  Score 1653;  DB 3;  Length 312;
     Best Local Similarity 100.0%;  Pred. No. 3.7e-151;
RESULT 692
ID   ABB97473 standard; protein; 328 AA.
DE   Novel human protein SEQ ID NO: 741.
PN   WO200222660-A2.
PD   21-MAR-2002.
PA   (HYSE-) HYSEQ INC.
     Query Match           78.6%;  Score 1392.5;  DB 5;  Length 328;
     Best Local Similarity  86.4%;  Pred. No. 7.3e-126;
RESULT 693
ID   ADS98765 standard; protein; 328 AA.
DE   Protein factor discovery related human contig polypeptide, SEQ ID 1029.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
     Query Match           78.6%;  Score 1392.5;  DB 8;  Length 328;
     Best Local Similarity  86.4%;  Pred. No. 7.3e-126;
RESULT 694
ID   ADS97998 standard; protein; 296 AA.
DE   Protein factor discovery related isolated human polypeptide, SEQ ID 262.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
     Query Match           76.1%;  Score 1349;  DB 8;  Length 296;
     Best Local Similarity 100.0%;  Pred. No. 1e-121;
RESULT 695
ID   AED97276 standard; protein; 227 AA.
DE   Human CS1 polypeptide #2.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match           67.7%;  Score 1199;  DB 9;  Length 227;
     Best Local Similarity 100.0%;  Pred. No. 2.5e-107;
RESULT 696
ID   AED97277 standard; protein; 227 AA.
DE   Chimpanzee CS1 polypeptide.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match           66.8%;  Score 1183;  DB 9;  Length 227;
     Best Local Similarity  98.2%;  Pred. No. 8.7e-106;
RESULT 697
ID   AED97274 standard; protein; 227 AA.
DE   Primate CS1 polypeptide.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match           60.3%;  Score 1069;  DB 9;  Length 227;
     Best Local Similarity  89.4%;  Pred. No. 9.9e-95;
RESULT 698
ID   AED97275 standard; protein; 227 AA.
DE   Rhesus monkey CS1 polypeptide.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.

     Query Match           59.9%;  Score 1061;  DB 9;  Length 227;
     Best Local Similarity  89.4%;  Pred. No. 5.9e-94;
RESULT 699
ID   AED97282 standard; protein; 227 AA.
DE   Chimeric human/murine CS1 polypeptide #5.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match           58.9%;  Score 1043;  DB 9;  Length 227;
     Best Local Similarity  88.7%;  Pred. No. 3.3e-92;
RESULT 700
ID   ADN02731 standard; protein; 204 AA.
DE   Human receptor and membrane -associated protein #34.
PN   WO2004029218-A2.
PD   08-APR-2004.
PA   (INCY/) INCYTE CORP.
     Query Match           56.3%;  Score 997.5;  DB 8;  Length 204;
     Best Local Similarity  60.9%;  Pred. No. 7.3e-88;
RESULT 701
ID   AED97279 standard; protein; 227 AA.
DE   Chimeric human/murine CS1 polypeptide #2.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match           55.4%;  Score 982;  DB 9;  Length 227;
     Best Local Similarity  82.8%;  Pred. No. 2.7e-86;
RESULT 702
ID   AED97280 standard; protein; 227 AA.
DE   Chimeric human/murine CS1 polypeptide #3.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match           54.3%;  Score 962;  DB 9;  Length 227;
     Best Local Similarity  82.4%;  Pred. No. 2.3e-84;
RESULT 703
ID   ABG11697 standard; protein; 684 AA.
DE   Novel human diagnostic protein #11688.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match           52.7%;  Score 933.5;  DB 4;  Length 684;
     Best Local Similarity  64.9%;  Pred. No. 6.8e-81;
RESULT 704
ID   ABG12169 standard; protein; 684 AA.
DE   Novel human diagnostic protein #12160.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match           52.7%;  Score 933.5;  DB 4;  Length 684;
     Best Local Similarity  64.9%;  Pred. No. 6.8e-81;
RESULT 705
ID   ADS98714 standard; protein; 684 AA.
DE   Protein factor discovery related human contig polypeptide, SEQ ID 978.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
     Query Match           52.7%;  Score 933.5;  DB 8;  Length 684;
     Best Local Similarity  64.9%;  Pred. No. 6.8e-81;
RESULT 706
ID   AED97281 standard; protein; 224 AA.
DE   Chimeric human/murine CS1 polypeptide #4.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match           47.3%;  Score 838.5;  DB 9;  Length 224;
     Best Local Similarity  71.4%;  Pred. No. 2.2e-72;
RESULT 707
ID   AED97278 standard; protein; 227 AA.
DE   Chimeric human/murine CS1 polypeptide #1.
PN   WO2005102387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
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Query Match           46.2%;    Score 818.5;  DB 9;  Length 224;
Best Local Similarity 70.6%;    Pred. No. 1.9e-70;
RESULT 708
ID   AED97283 standard; protein; 224 AA.
DE   Chimeric human/murine CS1 polypeptide #6.
PN   WO200510387-A2.
PD   03-NOV-2005.
PA   (PROT-) PROTEIN DESIGN LABS INC.
Query Match           42.7%;    Score 757.5;  DB 9;  Length 224;
Best Local Similarity 65.2%;    Pred. No. 1.6e-64;
RESULT 709
ID   ADR20055 standard; protein; 165 AA.
DE   Human immune response associated protein (IRAP), seq id 15.
PN   WO2004048550-A2.
PD   10-JUN-2004.
PA   (INCY-) INCYTE CORP.
Query Match           36.9%;    Score 653;  DB 8;  Length 165;
Best Local Similarity 90.9%;    Pred. No. 1.3e-54;
RESULT 710
ID   AAY12645 standard; protein; 124 AA.
DE   Human 5' EST secreted protein SEQ ID NO: 310 from WO 9906553.
PN   WO9906553-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
Query Match           35.1%;    Score 622;  DB 2;  Length 124;
Best Local Similarity 97.6%;    Pred. No. 9e-52;
RESULT 711
ID   AAW67811 standard; protein; 110 AA.
DE   Human secreted protein encoded by gene 5 clone HASAV70.
PN   WO9842738-A1.
PD   01-OCT-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           32.8%;    Score 582;  DB 3;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 712
ID   AAB32405 standard; protein; 110 AA.
DE   Human secreted protein sequence encoded by gene 3 SEQ ID NO:91.
PN   WO200047602-A1.
PD   17-AUG-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           32.8%;    Score 582;  DB 2;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 713
ID   ADA57321 standard; protein; 110 AA.
DE   Human secreted protein #32.
PN   WO2002102994-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           32.8%;    Score 582;  DB 6;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 714
ID   ADA56750 standard; protein; 110 AA.
DE   Human secreted protein #32.
PN   WO2002102994-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           32.8%;    Score 582;  DB 6;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 715
ID   ADA40601 standard; protein; 110 AA.
DE   Human secreted protein.
PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           32.8%;    Score 582;  DB 6;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 716
ID   ADA41198 standard; protein; 110 AA.
DE   Human secreted protein.
PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           32.8%;    Score 582;  DB 6;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 717
ID   AEL29531 standard; protein; 110 AA.
DE   Human secreted protein, SEQ ID 1511.
PN   US2006223088-A1.
PD   05-OCT-2006.
Query Match           32.8%;    Score 582;  DB 10;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 718
ID   AEL28959 standard; protein; 110 AA.
DE   Human secreted protein, SEQ ID 939.
PN   US2006223088-A1.
PD   05-OCT-2006.
Query Match           32.8%;    Score 582;  DB 10;  Length 110;
Best Local Similarity 100.0%;   Pred. No. 5.7e-48;
RESULT 719
ID   AAG00391 standard; protein; 97 AA.
DE   Human secreted protein, SEQ ID NO: 4472.
PN   EP103401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
Query Match           28.1%;    Score 498;  DB 3;  Length 97;
Best Local Similarity 100.0%;   Pred. No. 6.6e-40;
RESULT 720
ID   AAY11662 standard; protein; 98 AA.
DE   Human 5' EST secreted protein SEQ ID NO:314.
PN   WO9906439-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
Query Match           28.1%;    Score 498;  DB 2;  Length 98;
Best Local Similarity 100.0%;   Pred. No. 6.7e-40;
RESULT 721
ID   AAM21122 standard; protein; 91 AA.
DE   Peptide #7556 encoded by probe for measuring cervical gene expression.
PN   WO200157278-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match           26.6%;    Score 471;  DB 4;  Length 91;
Best Local Similarity 100.0%;   Pred. No. 2.5e-37;
RESULT 722
ID   ABB43438 standard; peptide; 91 AA.
DE   Peptide #10944 encoded by human foetal liver single exon probe.
PN   WO200157277-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match           26.6%;    Score 471;  DB 4;  Length 91;
Best Local Similarity 100.0%;   Pred. No. 2.5e-37;
RESULT 723
ID   AAM37326 standard; protein; 91 AA.
DE   Peptide #11363 encoded by probe for measuring placental gene expression.
PN   WO200157272-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match           26.6%;    Score 471;  DB 4;  Length 91;
Best Local Similarity 100.0%;   Pred. No. 2.5e-37;
RESULT 724
ID   ABB26408 standard; protein; 91 AA.
DE   Protein #8407 encoded by probe for measuring heart cell gene expression.
PN   WO200157274-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match           26.6%;    Score 471;  DB 4;  Length 91;
Best Local Similarity 100.0%;   Pred. No. 2.5e-37;
RESULT 725
ID   AAM77190 standard; protein; 91 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 37496.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
Query Match           26.6%;    Score 471;  DB 4;  Length 91;
Best Local Similarity 100.0%;   Pred. No. 2.5e-37;
RESULT 726
ID   AAM64367 standard; protein; 91 AA.
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DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 36472.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match             26.6%;  Score 471;  DB 4;  Length 91;
     Best Local Similarity   100.0%;  Pred. No. 2.5e-37;
RESULT 727
ID   ABG58815 standard; peptide; 91 AA.
DE   Human liver peptide, SEQ ID NO 37463.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match             26.6%;  Score 471;  DB 4;  Length 91;
     Best Local Similarity   100.0%;  Pred. No. 2.5e-37;
RESULT 728
ID   ABG46203 standard; peptide; 91 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 35868.
PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
     Query Match             26.6%;  Score 471;  DB 5;  Length 91;
     Best Local Similarity   100.0%;  Pred. No. 2.5e-37;
RESULT 729
ID   AAB32404 standard; protein; 90 AA.
DE   Human secreted protein sequence encoded by gene 3 SEQ ID NO:90.
PN   WO200047602-A1.
PD   17-AUG-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             25.1%;  Score 445;  DB 3;  Length 90;
     Best Local Similarity   100.0%;  Pred. No. 8.2e-35;
RESULT 730
ID   AAB47878 standard; protein; 328 AA.
DE   SCZ/CD84.
PN   WO200202054-A2.
PD   10-JAN-2002.
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
     Query Match             20.5%;  Score 362.5;  DB 5;  Length 328;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 731
ID   AAE26238 standard; protein; 328 AA.
DE   Human CD84 protein.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match             20.5%;  Score 362.5;  DB 5;  Length 328;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 732
ID   ADL82907 standard; protein; 328 AA.
DE   Human leukocyte differentiation antigen CD84.
PN   WO2004032867-A2.
PD   22-APR-2004.
PA   (TOLE-) TOLERRX INC.
     Query Match             20.5%;  Score 362.5;  DB 8;  Length 328;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 733
ID   ADQ19067 standard; protein; 328 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match             20.5%;  Score 362.5;  DB 8;  Length 328;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 734
ID   ADP23943 standard; protein; 328 AA.
DE   PRO polypeptide SEQ ID NO:1121.
PN   WO2004041170-A2.
PD   21-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match             20.5%;  Score 362.5;  DB 8;  Length 328;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 735
ID   ADY16548 standard; protein; 328 AA.
DE   PRO polypeptide SEQ ID NO 2354.
PN   WO200501962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match             20.5%;  Score 362.5;  DB 9;  Length 328;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 736
ID   ADY15656 standard; protein; 328 AA.
DE   PRO polypeptide SEQ ID NO 1462.
PN   WO200501962-A2.
PD   24-FEB-2005.
PA   (GETH ) GENENTECH INC.
     Query Match             20.5%;  Score 362.5;  DB 9;  Length 328;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 737
ID   AAW74891 standard; protein; 329 AA.
DE   Human secreted protein encoded by gene 164 clone HSAWF26.
PN   WO9839448-A2.
PD   11-SEP-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             20.5%;  Score 362.5;  DB 2;  Length 329;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 738
ID   ABG95343 standard; protein; 329 AA.
DE   Human novel secreted protein #164.
PN   US6420526-B1.
PD   16-JUL-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match             20.5%;  Score 362.5;  DB 5;  Length 329;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 739
ID   ABO34537 standard; protein; 329 AA.
DE   Region of human secreted protein encoded by cDNA sequence #164.
PN   US2003049618-A1.
PD   13-MAR-2003.
PA   (RUBE/) RUBEN S M.
PA   (ROSE/) ROSEN C A.
PA   (SOPP/) SOPPET D R.
PA   (CART/) CARTER K C.
PA   (BEDN/) BEDNARIK D P.
PA   (ENDR/) ENDRESS G A.
PA   (YUGG/) YU G.
PA   (NIJJ/) NI J.
PA   (FENG/) FENG P.
PA   (YOUN/) YOUNG P E.
PA   (GREE/) GREENE J M.
PA   (FERR/) FERRIE A M.
PA   (DUAN/) DUAN D R.
PA   (HUJJ/) HU J.
PA   (FLOR/) FLORENCE K A.
PA   (OLSE/) OLSEN H S.
PA   (FISC/) FISCHER C L.
PA   (EBNE/) EBNER R.
PA   (BREW/) BREWER L A.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (LAFL/) LAFLEUR D W.
PA   (LIYY/) LI Y.
PA   (ZENG/) ZENG Z.
PA   (KYAW/) KYAW H.
     Query Match             20.5%;  Score 362.5;  DB 6;  Length 329;
     Best Local Similarity   31.5%;  Pred. No. 5.4e-26;
RESULT 740
ID   ADI23198 standard; protein; 329 AA.
DE   Novel human secreted protein seq id 483.
PN   US2003175858-A1.
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PD   18-SEP-2003.
PA   (RUBE/)  RUBEN S M.
PA   (ROSE/)  ROSEN C A.
PA   (SOPP/)  SOPPET D R.
PA   (CART/)  CARTER K C.
PA   (BEDN/)  BEDNARIK D P.
PA   (ENDR/)  ENDRESS G A.
PA   (YUGG/)  YU G.
PA   (NIJJ/)  NI J.
PA   (FENG/)  FENG P.
PA   (YOUN/)  YOUNG P E.
PA   (GREE/)  GREENE J M.
PA   (FERR/)  FERRIE A M.
PA   (DUAN/)  DUAN D R.
PA   (HUJJ/)  HU J.
PA   (FLOR/)  FLORENCE K A.
PA   (OLSE/)  OLSEN H S.
PA   (FISC/)  FISCHER C L.
PA   (EBNE/)  EBNER R.
PA   (BREW/)  BREWER L A.
PA   (MOOR/)  MOORE P A.
PA   (SHIY/)  SHI Y.
PA   (LAFL/)  LAFLEUR D W.
PA   (LIYY/)  LI Y.
PA   (ZENG/)  ZENG Z.
PA   (KYAW/)  KYAW H.
     Query Match          20.5%;   Score 362.5;  DB 7;   Length 329;
     Best Local Similarity 31.5%;   Pred. No. 5.4e-26;
RESULT 742
ID   ADH74200 standard; protein; 329 AA.
DE   Human secreted protein #164.
PN   US2003225248-A1.
PD   04-DEC-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
RESULT 743
ID   AEH06032 standard; protein; 329 AA.
DE   Human disease dagnosis / therapy related polypeptide SEQ ID NO: 483.
PN   US2006084082-A1.
PD   20-APR-2006.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match          20.5%;   Score 362.5;  DB 8;   Length 329;
     Best Local Similarity 31.5%;   Pred. No. 5.4e-26;
RESULT 744
ID   AAU74424 standard; protein; 629 AA.
DE   Mouse protein sequence #3, related to isolation of genes within SLE-1B.
PN   WO200188200-A2.
PD   22-NOV-2001.
PA   (TEXA ) UNIV TEXAS SYSTEM.
     Query Match          20.5%;   Score 362.5;  DB 10;  Length 329;
     Best Local Similarity 31.5%;   Pred. No. 5.4e-26;
RESULT 745
ID   AAE26250 standard; protein; 289 AA.
DE   Human CD2001 protein #2.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          19.4%;   Score 343;    DB 5;   Length 629;
     Best Local Similarity 29.3%;   Pred. No. 1.1e-23;
RESULT 746
ID   ABW01830 standard; protein; 289 AA.
DE   Human CD2001 protein #3.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.8%;   Score 333.5;  DB 5;   Length 289;
     Best Local Similarity 31.0%;   Pred. No. 2.9e-23;
RESULT 747
ID   AAE12078 standard; protein; 289 AA.
DE   Dendritic cell (DC) DCLYR protein.
PN   WO200172773-A2.
PD   04-OCT-2001.

PD   18-SEP-2003.
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
     Query Match          18.7%;   Score 330.5;  DB 4;   Length 289;
     Best Local Similarity 30.6%;   Pred. No. 5.7e-23;
RESULT 748
ID   AAE26243 standard; protein; 289 AA.
DE   Human CD2001 protein.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.7%;   Score 330.5;  DB 5;   Length 289;
     Best Local Similarity 30.6%;   Pred. No. 5.7e-23;
RESULT 749
ID   AAE26253 standard; protein; 289 AA.
DE   Human CD2001 protein #5.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.7%;   Score 330.5;  DB 5;   Length 289;
     Best Local Similarity 30.6%;   Pred. No. 5.7e-23;
RESULT 750
ID   ABP65110 standard; protein; 289 AA.
DE   Hypoxia-induced protein #36.
PN   WO200246465-A2.
PD   13-JUN-2002.
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
     Query Match          18.7%;   Score 330.5;  DB 5;   Length 289;
     Best Local Similarity 30.6%;   Pred. No. 5.7e-23;
RESULT 751
ID   ABW01823 standard; protein; 289 AA.
DE   Human CD2001 protein #1.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.7%;   Score 330.5;  DB 7;   Length 289;
     Best Local Similarity 30.6%;   Pred. No. 5.7e-23;
RESULT 752
ID   ABW01833 standard; protein; 289 AA.
DE   Human CD2001 protein #6.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.7%;   Score 330.5;  DB 7;   Length 289;
     Best Local Similarity 30.6%;   Pred. No. 5.7e-23;
RESULT 753
ID   AAE26251 standard; protein; 289 AA.
DE   Human CD2001 protein #3.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.5%;   Score 327.5;  DB 5;   Length 289;
     Best Local Similarity 30.3%;   Pred. No. 1.1e-22;
RESULT 754
ID   AAE26252 standard; protein; 289 AA.
DE   Human CD2001 protein #4.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.5%;   Score 327.5;  DB 5;   Length 289;
     Best Local Similarity 30.3%;   Pred. No. 1.1e-22;
RESULT 755
ID   ABW01831 standard; protein; 289 AA.
DE   Human CD2001 protein #4.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match          18.5%;   Score 327.5;  DB 7;   Length 289;
     Best Local Similarity 30.3%;   Pred. No. 1.1e-22;
RESULT 756
ID   ABW01832 standard; protein; 289 AA.
DE   Human CD2001 protein #5.
PN   US2003180888-A1.
PD   25-SEP-2003.
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PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           18.5%;   Score 327.5;   DB 7;   Length 289;
Best Local Similarity 30.3%;   Pred. No. 1.1e-22;
RESULT 757
ID   AAE26244 standard; protein; 270 AA.
DE   Human CD2001 mature protein.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           18.5%;   Score 327;   DB 5;   Length 270;
Best Local Similarity 31.4%;   Pred. No. 1.1e-22;
RESULT 758
ID   ABW01824 standard; protein; 270 AA.
DE   Human CD2001 mature protein.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           18.5%;   Score 327;   DB 7;   Length 270;
Best Local Similarity 31.4%;   Pred. No. 1.1e-22;
RESULT 759
ID   ADS98002 standard; protein; 632 AA.
DE   Protein factor discovery related isolated human polypeptide, SEQ ID 266.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
Query Match           18.2%;   Score 323;   DB 8;   Length 632;
Best Local Similarity 30.3%;   Pred. No. 9.6e-22;
RESULT 760
ID   ADS97999 standard; protein; 655 AA.
DE   Protein factor discovery related isolated human polypeptide, SEQ ID 263.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
Query Match           18.2%;   Score 323;   DB 8;   Length 655;
Best Local Similarity 30.3%;   Pred. No. 1e-21;
RESULT 761
ID   ADS98003 standard; protein; 669 AA.
DE   Protein factor discovery related isolated human polypeptide, SEQ ID 267.
PN   WO2004087874-A2.
PD   14-OCT-2004.
PA   (NUVE-) NUVELO INC.
PA   (DRMA/) DRMANAC R T.
Query Match           18.2%;   Score 323;   DB 8;   Length 669;
Best Local Similarity 30.3%;   Pred. No. 1e-21;
RESULT 762
ID   AAE26239 standard; protein; 331 AA.
DE   Human CD2000 protein #3.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           18.0%;   Score 319.5;   DB 5;   Length 331;
Best Local Similarity 29.9%;   Pred. No. 8.1e-22;
RESULT 763
ID   ABW01818 standard; protein; 331 AA.
DE   Human CD2000 protein #2.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           18.0%;   Score 319.5;   DB 7;   Length 331;
Best Local Similarity 29.9%;   Pred. No. 8.1e-22;
RESULT 764
ID   ADL57103 standard; protein; 615 AA.
DE   Human NOV5a protein SEQ ID NO:48.
PN   WO2004022723-A2.
PD   18-MAR-2004.
PA   (CURA-) CURAGEN CORP.
Query Match           17.9%;   Score 318;   DB 8;   Length 615;
Best Local Similarity 30.3%;   Pred. No. 2.8e-21;
RESULT 765
ID   AD063782 standard; protein; 654 AA.
DE   Human Ly-9 polypeptide.

PN   US2004109862-A1.
PD   10-JUN-2004.
PA   (EMTA/) EMTAGE P C R.
Query Match           17.9%;   Score 318;   DB 8;   Length 654;
Best Local Similarity 30.3%;   Pred. No. 3.1e-21;
RESULT 766
ID   AD078174 standard; protein; 654 AA.
DE   Human Ly-9 polypeptide.
PN   US2004109863-A1.
PD   10-JUN-2004.
PA   (EMTA/) EMTAGE P.
Query Match           17.9%;   Score 318;   DB 8;   Length 654;
Best Local Similarity 30.3%;   Pred. No. 3.1e-21;
RESULT 767
ID   ADK41513 standard; protein; 331 AA.
DE   Anti-cell surface antigen related protein #1.
PN   WO2003066935-A2.
PD   21-AUG-2003.
PA   (NUVE-) NUVELO INC.
Query Match           17.9%;   Score 316.5;   DB 7;   Length 331;
Best Local Similarity 29.6%;   Pred. No. 1.6e-21;
RESULT 768
ID   AEH34100 standard; protein; 331 AA.
DE   Human CD84Hy1 protein coding sequence - SEQ ID 2.
PN   US2006104977-A1.
PD   18-MAY-2006.
PA   (NUVE-) NUVELO INC.
Query Match           17.9%;   Score 316.5;   DB 10;   Length 331;
Best Local Similarity 29.6%;   Pred. No. 1.6e-21;
RESULT 769
ID   AAE26222 standard; protein; 309 AA.
DE   Human CD2000 mature protein.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           17.8%;   Score 315.5;   DB 5;   Length 309;
Best Local Similarity 29.6%;   Pred. No. 1.8e-21;
RESULT 770
ID   ABW01801 standard; protein; 309 AA.
DE   Human CD2000 mature protein.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           17.8%;   Score 315.5;   DB 7;   Length 309;
Best Local Similarity 29.6%;   Pred. No. 1.8e-21;
RESULT 771
ID   ABB90183 standard; protein; 331 AA.
DE   Human polypeptide SEQ ID NO 2559.
PN   WO200190304-A2.
PD   29-NOV-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match           17.8%;   Score 315.5;   DB 5;   Length 331;
Best Local Similarity 29.6%;   Pred. No. 2e-21;
RESULT 772
ID   AAE26220 standard; protein; 331 AA.
DE   Human CD2000 protein.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
Query Match           17.8%;   Score 315.5;   DB 5;   Length 331;
Best Local Similarity 29.6%;   Pred. No. 2e-21;
RESULT 773
ID   ABR39107 standard; protein; 331 AA.
DE   Human NTB-A protein SEQ ID NO:2.
PN   WO2003008449-A1.
PD   30-JAN-2003.
PA   (INNA-) INNATE PHARMA.
PA   (UYGE-) UNIV GENOVA.
Query Match           17.8%;   Score 315.5;   DB 6;   Length 331;
Best Local Similarity 29.6%;   Pred. No. 2e-21;
RESULT 774
ID   ABU03145 standard; protein; 331 AA.
DE   Human immunoglobulin (Ig) APEX4 protein.
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PN WO200277173-A2.
PD 03-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
   Query Match   17.8%; Score 315.5; DB 6; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 775
ID ADC52556 standard; protein; 331 AA.
DE human dendritic cell membrane protein #SEQ ID 9.
PN JP2003052374-A.
PD 25-FEB-2003.
PA (KIRI) KIRIN BREWERY KK.
   Query Match   17.8%; Score 315.5; DB 7; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 776
ID ABW01799 standard; protein; 331 AA.
DE Human CD2000 protein #1.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
   Query Match   17.8%; Score 315.5; DB 7; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 777
ID ADI37022 standard; protein; 331 AA.
DE Novel human secreted and transmembrane protein PRO 71240.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (GETH) GENENTECH INC.
   Query Match   17.8%; Score 315.5; DB 7; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 778
ID ADQ66345 standard; protein; 331 AA.
DE Novel human protein sequence #1318.
PN EP1449962-A2.
PD 15-JAN-2004.
PA (REAS) RES ASSOC BIOTECHNOLOGY.
   Query Match   17.8%; Score 315.5; DB 8; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 779
ID ADY19430 standard; protein; 331 AA.
DE PRO polypeptide SEQ ID NO 5236.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
   Query Match   17.8%; Score 315.5; DB 8; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 780
ID ADZ13231 standard; protein; 331 AA.
DE Human cancer-associated protein #235.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
   Query Match   17.8%; Score 315.5; DB 9; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 781
ID AEB98756 standard; protein; 331 AA.
DE Human dendritic cell membrane molecule, SEQ ID 2.
PN JP2005206478-A.
PD 04-AUG-2005.
PA (KIRI) KIRIN BREWERY KK.
   Query Match   17.8%; Score 315.5; DB 9; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2e-21;
RESULT 782
ID AAU09868 standard; protein; 346 AA.
DE Novel human secreted protein #9.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
   Query Match   17.8%; Score 315.5; DB 5; Length 346;
   Best Local Similarity 29.6%; Pred. No. 2.1e-21;
RESULT 783
ID AAE26241 standard; protein; 331 AA.
DE Human CD2000 protein #5.

PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
   Query Match   17.7%; Score 314.5; DB 5; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2.5e-21;
RESULT 784
ID ABW01820 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
   Query Match   17.7%; Score 314.5; DB 7; Length 331;
   Best Local Similarity 29.6%; Pred. No. 2.5e-21;
RESULT 785
ID AAE26240 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
   Query Match   17.7%; Score 313.5; DB 5; Length 331;
   Best Local Similarity 29.6%; Pred. No. 3.1e-21;
RESULT 786
ID ABW01819 standard; protein; 331 AA.
DE Human CD2000 protein #3.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
   Query Match   17.7%; Score 313.5; DB 7; Length 331;
   Best Local Similarity 29.6%; Pred. No. 3.1e-21;
RESULT 787
ID AAU74425 standard; protein; 610 AA.
DE Human protein sequence #3, related to isolation of genes within SLE-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
   Query Match   17.6%; Score 312.5; DB 5; Length 610;
   Best Local Similarity 25.7%; Pred. No. 9.5e-21;
RESULT 788
ID ADS98001 standard; protein; 641 AA.
DE Protein factor discovery related isolated human polypeptide, SEQ ID 265.
PN WO2004087874-A2.
PD 14-OCT-2004.
PA (NUVE-) NUVELO INC.
PA (DRMA/) DRMANAC R T.
   Query Match   17.6%; Score 312.5; DB 8; Length 641;
   Best Local Similarity 25.7%; Pred. No. 1e-20;
RESULT 789
ID AAE26242 standard; protein; 331 AA.
DE Human CD2000 protein #6.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
   Query Match   17.6%; Score 311.5; DB 5; Length 331;
   Best Local Similarity 29.6%; Pred. No. 4.8e-21;
RESULT 790
ID ABW01821 standard; protein; 331 AA.
DE Human CD2000 protein #5.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
   Query Match   17.6%; Score 311.5; DB 7; Length 331;
   Best Local Similarity 29.6%; Pred. No. 4.8e-21;
RESULT 791
ID AAG63166 standard; protein; 332 AA.
DE Amino acid sequence of a CD84-like polypeptide.
PN WO200155336-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
   Query Match   17.6%; Score 311; DB 4; Length 332;
   Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 792
ID ABG96267 standard; protein; 332 AA.
DE Human immunoglobulin superfamily protein IGSFP-5.

PN   WO200272794-A2.
PD   19-SEP-2002.
PA   (INCY-) INCYTE GENOMICS INC.
     Query Match   17.6%;   Score 311;   DB 5;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
ID   ABG34067 standard; protein; 332 AA.
DE   Human Pro peptide #38.
PN   WO20022488-A2.
PD   28-MAR-2002.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 5;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 794
ID   ABU03170 standard; protein; 332 AA.
DE   Human immunoglobulin (Ig) APEX4v1 protein.
PN   WO200277173-A2.
PD   03-OCT-2002.
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
     Query Match   17.6%;   Score 311;   DB 6;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 795
ID   ADA37159 standard; protein; 332 AA.
DE   Human PRO20080 protein SEQ ID NO:2.
PN   WO2003055440-A2.
PD   10-JUL-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 6;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 796
ID   ADA01344 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003068779-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 6;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 797
ID   ADA43773 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003064474-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 6;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 798
ID   ADA43541 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003073196-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 6;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 799
ID   ADA01216 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003068782-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 6;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 800
ID   ADA01100 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003068780-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 801
ID   ADA43657 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003073190-A1.

PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 802
ID   ADA06919 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003068781-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 803
ID   ADA08407 standard; protein; 332 AA.
DE   Novel human secreted and transmembrane protein PRO20080.
PN   US2003068783-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 804
ID   ADB99700 standard; protein; 332 AA.
DE   Human PRO polypeptide SEQ ID 76.
PN   US2003082728-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 805
ID   ADB86983 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003082726-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 806
ID   ADB66138 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003082729-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 807
ID   ADB99816 standard; protein; 332 AA.
DE   Human PRO polypeptide SEQ ID 76.
PN   US2003073192-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 808
ID   ADB99471 standard; protein; 332 AA.
DE   Novel human secreted and transmembrane protein PRO20080.
PN   US2003082731-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 809
ID   ADB66022 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003082732-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   17.6%;   Score 311;   DB 7;   Length 332;
     Best Local Similarity   29.9%;   Pred. No. 5.4e-21;
RESULT 810
ID   ADC23420 standard; protein; 332 AA.
DE   Human transmembrane PRO polypeptide (SeqID 76).
PN   US2003073193-A1.
PD   17-APR-2003.

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PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 811
ID   ADC26113 standard; protein; 332 AA.
DE   Human PRO20080 protein.
PN   US2003073194-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 812
ID   ADE04940 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003068778-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 813
ID   ADE11246 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003073191-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 814
ID   ADD88177 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003082733-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 815
ID   ADD95472 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003064473-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 816
ID   ADE06402 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003073195-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 817
ID   ADE38177 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003119120-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 818
ID   ADD88293 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003073189-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 819
ID   ADD90874 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003073188-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.

     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 820
ID   ADF99429 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003078401-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 821
ID   ADG06522 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003077742-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 822
ID   ADG05473 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003077741-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 823
ID   ADG82474 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003077744-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 7;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 824
ID   ADE51727 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003104560-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 8;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 825
ID   ADE51843 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003104561-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 8;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 826
ID   ADE37701 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003104564-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 8;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 827
ID   ADE37585 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003104565-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 8;  Length 332;
     Best Local Similarity   29.9%;  Pred. No. 5.4e-21;
RESULT 828
ID   ADD95356 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003138901-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             17.6%;  Score 311;  DB 8;  Length 332;
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  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 829
ID   ADE52379 standard; protein; 332 AA.
DE   Human PRO20080.
PN   US2003099661-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 830
ID   ADE38056 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003104566-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 831
ID   ADE76145 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003124665-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 832
ID   ADE39468 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003119117-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 833
ID   ADE04272 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003096364-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 834
ID   ADE39869 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003138896-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 835
ID   ADE19734 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003138903-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 836
ID   ADE77312 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003124666-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 837
ID   ADE65420 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003119116-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;


RESULT 838
ID   ADE76029 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003124663-A1.
PD   03-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 839
ID   ADE37940 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003119119-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 840
ID   ADE64550 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003119114-A1.
PD   26-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 841
ID   ADE38885 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003096363-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 842
ID   ADE51959 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003104562-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 843
ID   ADD90990 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003138902-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 844
ID   ADE38769 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003108996-A1.
PD   12-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 845
ID   ADE37469 standard; protein; 332 AA.
DE   Human secreted/transmembrane polypeptide PRO20080.
PN   US2003104563-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 846
ID   ADE06286 standard; protein; 332 AA.
DE   Human PRO polypeptide #38.
PN   US2003138898-A1.
PD   24-JUL-2003.
PA   (GETH ) GENENTECH INC.
  Query Match  17.6%;  Score 311;  DB 8;  Length 332;
  Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 847
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ID  ADD90145 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003138904-A1.
PD  24-JUL-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 848
ID  ADE38653 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003119086-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 849
ID  ADE39584 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003119118-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 850
ID  ADD89189 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003138897-A1.
PD  24-JUL-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 851
ID  ADD88956 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003138899-A1.
PD  24-JUL-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 852
ID  ADE19850 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003138900-A1.
PD  24-JUL-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 853
ID  ADE77428 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003124667-A1.
PD  03-JUL-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 854
ID  ADE65304 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003119113-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 855
ID  ADE39952 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003119115-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 856
ID  ADE38837 standard; protein; 332 AA.

DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003104555-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 857
ID  ADG11090 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003170809-A1.
PD  11-SEP-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 858
ID  ADG10974 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003077743-A1.
PD  24-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 859
ID  ADH31502 standard; protein; 332 AA.
DE  Human PRO polypeptide #38.
PN  US2003119139-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 860
ID  ADH38750 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003119140-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 861
ID  ADH29385 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003119137-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 862
ID  ADH23688 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003119143-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 863
ID  ADH27018 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
PN  US2003119115-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 864
ID  ADH38286 standard; protein; 332 AA.
DE  Novel human secreted and transmembrane protein PRO20080.
PN  US2003119124-A1.
PD  26-JUN-2003.
PA  (GETH ) GENENTECH INC.
    Query Match          17.6%;   Score 311;  DB 8;   Length 332;
    Best Local Similarity 29.9%;   Pred. No. 5.4e-21;
RESULT 865
ID  ADH26902 standard; protein; 332 AA.
DE  Human secreted/transmembrane polypeptide PRO20080.
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PN US2003119134-A1
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 866
ID ADH38170 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 867
ID ADH38866 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 868
ID ADH23804 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 869
ID ADH40179 standard; protein; 332 AA.
DE Human PRO20080 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 870
ID ADH40064 standard; protein; 332 AA.
DE Human PRO20080 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 871
ID ADH31386 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 872
ID ADH29264 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 873
ID ADH49479 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 874
ID ADH51943 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119125-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 875
ID ADH49798 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 876
ID ADH52399 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 877
ID ADH52515 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 878
ID ADH58512 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 879
ID ADH51827 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 880
ID ADH58388 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 881
ID ADI13585 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 882
ID ADK00841 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 5.4e-21;
RESULT 883
ID ADL08582 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003186372-A1.
PD 02-OCT-2003.

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PA    (GETH ) GENENTECH INC.
      Query Match            17.6%;  Score 311;  DB 8;  Length 332;
      Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 884
ID    ADS10567 standard; protein; 332 AA.
DE    Human therapeutic protein - SEQ ID 804.
PN    WO200408148-A2.
PD    23-SEP-2004.
PA    (NUVE-) NUVELO INC.
      Query Match            17.6%;  Score 311;  DB 8;  Length 332;
      Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 885
ID    AEG75242 standard; protein; 332 AA.
DE    Human PRO20080 protein.
PN    US2006073579-A1.
PD    06-APR-2006.
PA    (GETH ) GENENTECH INC.
      Query Match            17.6%;  Score 311;  DB 10;  Length 332;
      Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 886
ID    AEG74457 standard; protein; 332 AA.
DE    Human PRO20080 protein SEQ ID NO:76.
PN    US2006073553-A1.
PD    06-APR-2006.
PA    (GETH ) GENENTECH INC.
      Query Match            17.6%;  Score 311;  DB 10;  Length 332;
      Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 887
ID    AEG73329 standard; protein; 332 AA.
DE    Human PRO20080 protein.
PN    US2006073551-A1.
PD    06-APR-2006.
PA    (GETH ) GENENTECH INC.
      Query Match            17.6%;  Score 311;  DB 10;  Length 332;
      Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 888
ID    AEG74573 standard; protein; 332 AA.
DE    Human PRO20080 polypeptide SEQ ID NO:76.
PN    US2006073552-A1.
PD    06-APR-2006.
PA    (GETH ) GENENTECH INC.
      Query Match            17.6%;  Score 311;  DB 10;  Length 332;
      Best Local Similarity  29.9%;  Pred. No. 5.4e-21;
RESULT 889
ID    ADY16550 standard; protein; 280 AA.
DE    PRO polypeptide SEQ ID NO 2356.
PN    WO200516962-A2.
PD    24-FEB-2005.
PA    (GETH ) GENENTECH INC.
      Query Match            17.4%;  Score 308;  DB 9;  Length 280;
      Best Local Similarity  32.3%;  Pred. No. 8.3e-21;
RESULT 890
ID    AAE26249 standard; protein; 236 AA.
DE    Human CD2001 protein #1.
PN    EP1223218-A1.
PD    17-JUL-2002.
PA    (MILL-) MILLENNIUM PHARM INC.
      Query Match            17.0%;  Score 301.5;  DB 5;  Length 236;
      Best Local Similarity  32.6%;  Pred. No. 2.7e-20;
RESULT 891
ID    ABW01829 standard; protein; 236 AA.
DE    Human CD2001 protein #2.
PN    US2003180888-A1.
PD    25-SEP-2003.
PA    (MILL-) MILLENNIUM PHARM INC.
      Query Match            17.0%;  Score 301.5;  DB 7;  Length 236;
      Best Local Similarity  32.6%;  Pred. No. 2.7e-20;
RESULT 892
ID    AAE26246 standard; protein; 217 AA.
DE    Human CD2001 protein transmembrane domain.
PN    EP1223218-A1.
PD    17-JUL-2002.
PA    (MILL-) MILLENNIUM PHARM INC.

      Query Match            16.8%;  Score 298;  DB 5;  Length 217;
      Best Local Similarity  33.8%;  Pred. No. 5.3e-20;
RESULT 893
ID    ABW01826 standard; protein; 217 AA.
DE    Human CD2001 protein extracellular domain.
PN    US2003180888-A1.
PD    25-SEP-2003.
PA    (MILL-) MILLENNIUM PHARM INC.
      Query Match            16.8%;  Score 298;  DB 7;  Length 217;
      Best Local Similarity  33.8%;  Pred. No. 5.3e-20;
RESULT 894
ID    ABG96270 standard; protein; 551 AA.
DE    Human immunoglobulin superfamily protein IGSFP-8.
PN    WO200272794-A2.
PD    19-SEP-2002.
PA    (INCY-) INCYTE GENOMICS INC.
      Query Match            16.8%;  Score 294.5;  DB 5;  Length 551;
      Best Local Similarity  30.4%;  Pred. No. 4.5e-19;
RESULT 895
ID    ADK98560 standard; protein; 565 AA.
DE    Human immune response associated protein IRAP-23 protein.
PN    WO200420593-A2.
PD    11-MAR-2004.
PA    (INCY-) INCYTE CORP.
      Query Match            16.6%;  Score 294.5;  DB 8;  Length 565;
      Best Local Similarity  30.4%;  Pred. No. 4.7e-19;
RESULT 896
ID    ADS98832 standard; protein; 284 AA.
DE    Protein factor discovery related human contig polypeptide, SEQ ID 1096.
PN    WO200487874-A2.
PD    14-OCT-2004.
PA    (NUVE-) NUVELO INC.
      (DRMA/) DRMANAC R T.
      Query Match            16.5%;  Score 291.5;  DB 8;  Length 284;
      Best Local Similarity  32.3%;  Pred. No. 3.4e-19;
RESULT 897
ID    AEA20174 standard; protein; 284 AA.
DE    Novel human polypeptide SEQ ID NO 868.
PN    WO2005049806-A2.
PD    02-JUN-2005.
PA    (NUVE-) NUVELO INC.
      Query Match            16.5%;  Score 291.5;  DB 9;  Length 284;
      Best Local Similarity  32.3%;  Pred. No. 3.4e-19;
RESULT 898
ID    ADL57243 standard; protein; 526 AA.
DE    Human NOV5c protein SEQ ID NO:188.
PN    WO200402723-A2.
PD    18-MAR-2004.
PA    (CURA-) CURAGEN CORP.
      Query Match            15.9%;  Score 282.5;  DB 8;  Length 526;
      Best Local Similarity  31.5%;  Pred. No. 6.2e-18;
RESULT 899
ID    ADL57105 standard; protein; 526 AA.
DE    Human NOV5b protein SEQ ID NO:50.
PN    WO200402723-A2.
PD    18-MAR-2004.
PA    (CURA-) CURAGEN CORP.
      Query Match            15.9%;  Score 282.5;  DB 8;  Length 526;
      Best Local Similarity  31.5%;  Pred. No. 6.2e-18;
RESULT 900
ID    ADR20041 standard; protein; 91 AA.
DE    Human immune response associated protein (IRAP), seq id 1.
PN    WO200448550-A2.
PD    10-JUN-2004.
PA    (INCY-) INCYTE CORP.
      Query Match            15.3%;  Score 272;  DB 8;  Length 91;
      Best Local Similarity  100.0%;  Pred. No. 4.9e-18;
RESULT 901
ID    ADZ13233 standard; protein; 271 AA.
DE    Human cancer-associated protein #236.
PN    WO200503101-A2.
PD    07-APR-2005.
PA    (CHIR ) CHIRON CORP.
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Query Match                    15.1%;   Score 267; DB 9;   Length 271;
Best Local Similarity          31.2%;   Pred. No. 7.5e-17;
RESULT 902
ID    ADZ13235 standard; protein; 317 AA.
DE    Human cancer-associated protein #237.
PN    WO2005031001-A2.
PD    07-APR-2005.
PA    (CHIR ) CHIRON CORP.
RESULT 903
Query Match                    14.8%;   Score 263; DB 9;   Length 317;
Best Local Similarity          31.0%;   Pred. No. 2.3e-16;
ID    AEB98758 standard; protein; 445 AA.
DE    Dendritic cell membrane molecule-immunoglobulin (Ig)Fc fusion protein.
PN    JP2005206478-A.
PD    04-AUG-2005.
PA    (KIRI ) KIRIN BREWERY KK.
RESULT 904
Query Match                    14.3%;   Score 254; DB 9;   Length 445;
Best Local Similarity          29.1%;   Pred. No. 2.8e-15;
ID    AAU09867 standard; protein; 220 AA.
DE    Novel human secreted protein #8.
PN    WO200179454-A1.
PD    25-OCT-2001.
PA    (SMIK ) SMITHKLINE BEECHAM CORP.
PA    (SMIK ) SMITHKLINE BEECHAM PLC.
RESULT 905
Query Match                    14.2%;   Score 251; DB 5;   Length 220;
Best Local Similarity          35.4%;   Pred. No. 2e-15;
ID    ABB53269 standard; protein; 310 AA.
DE    Human polypeptide #9.
PN    WO200181363-A1.
PD    01-NOV-2001.
PA    (SMIK ) SMITHKLINE BEECHAM CORP.
PA    (SMIK ) SMITHKLINE BEECHAM PLC.
RESULT 906
Query Match                    13.9%;   Score 247; DB 5;   Length 310;
Best Local Similarity          26.7%;   Pred. No. 7.9e-15;
ID    AAE26231 standard; protein; 195 AA.
DE    Human CD2000 protein #2.
PN    EP1223218-A1.
PD    17-JUL-2002.
PA    (MILL-) MILLENNIUM PHARM INC.
RESULT 907
Query Match                    13.8%;   Score 245; DB 5;   Length 195;
Best Local Similarity          35.1%;   Pred. No. 6.3e-15;
ID    ABW01810 standard; protein; 195 AA.
DE    Human CD2000 protein extracellular domain #4.
PN    US2003180888-A1.
PD    25-SEP-2003.
PA    (MILL-) MILLENNIUM PHARM INC.
RESULT 908
Query Match                    13.8%;   Score 245; DB 7;   Length 195;
Best Local Similarity          35.1%;   Pred. No. 6.3e-15;
ID    AAE26232 standard; protein; 203 AA.
DE    Human CD2000 protein transmembrane domain.
PN    EP1223218-A1.
PD    17-JUL-2002.
PA    (MILL-) MILLENNIUM PHARM INC.
RESULT 909
Query Match                    13.8%;   Score 245; DB 5;   Length 203;
Best Local Similarity          35.1%;   Pred. No. 6.6e-15;
ID    ABW01811 standard; protein; 203 AA.
DE    Human CD2000 protein extracellular domain #5.
PN    US2003180888-A1.
PD    25-SEP-2003.
PA    (MILL-) MILLENNIUM PHARM INC.
RESULT 910
Query Match                    13.8%;   Score 245; DB 7;   Length 203;
Best Local Similarity          35.1%;   Pred. No. 6.6e-15;
ID    AEA23943 standard; protein; 423 AA.
DE    Human PRO polypeptide SEQ ID NO 485.
PN    WO2005051988-A2.
PD    09-JUN-2005.
PA    (GETH ) GENENTECH INC.
Query Match                    13.5%;   Score 238.5; DB 9;   Length 423;
Best Local Similarity          32.1%;   Pred. No. 8.3e-14;
RESULT 911
ID    ABB53268 standard; protein; 229 AA.
DE    Human polypeptide #8.
PN    WO200181363-A1.
PD    01-NOV-2001.
PA    (SMIK ) SMITHKLINE BEECHAM CORP.
PA    (SMIK ) SMITHKLINE BEECHAM PLC.
Query Match                    13.3%;   Score 236.5; DB 5;   Length 229;
Best Local Similarity          28.6%;   Pred. No. 5.3e-14;
RESULT 912
ID    ADZ13228 standard; protein; 331 AA.
DE    Murine cancer-associated protein #79.
PN    WO2005031001-A2.
PD    07-APR-2005.
PA    (CHIR ) CHIRON CORP.
Query Match                    12.7%;   Score 225.5; DB 9;   Length 331;
Best Local Similarity          26.0%;   Pred. No. 1.1e-12;
RESULT 913
ID    AAB47322 standard; protein; 351 AA.
DE    APEX-2.
PN    WO200146260-A2.
PD    28-JUN-2001.
PA    (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match                    12.7%;   Score 225.5; DB 4;   Length 351;
Best Local Similarity          26.0%;   Pred. No. 1.2e-12;
RESULT 914
ID    ABB89245 standard; protein; 168 AA.
DE    Human polypeptide SEQ ID NO 1621.
PN    WO200190304-A2.
PD    29-NOV-2001.
PA    (HUMA-) HUMAN GENOME SCI INC.
Query Match                    12.4%;   Score 219; DB 5;   Length 168;
Best Local Similarity          32.3%;   Pred. No. 1.7e-12;
RESULT 915
ID    ABU03171 standard; protein; 220 AA.
DE    Human immunoglobulin (Ig) APEX4sv1 protein.
PN    WO200277173-A2.
PD    03-OCT-2002.
PA    (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match                    11.6%;   Score 206; DB 6;   Length 220;
Best Local Similarity          28.3%;   Pred. No. 4.5e-11;
RESULT 916
ID    AAE26225 standard; protein; 159 AA.
DE    Human CD2000 protein #1.
PN    EP1223218-A1.
PD    17-JUL-2002.
PA    (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match                    11.3%;   Score 200.5; DB 5;   Length 159;
Best Local Similarity          35.2%;   Pred. No. 9.6e-11;
RESULT 917
ID    ABW01804 standard; protein; 159 AA.
DE    Human CD2000 protein cytoplasmic domain #1.
PN    US2003180888-A1.
PD    25-SEP-2003.
PA    (MILL-) MILLENNIUM PHARM INC.
Query Match                    11.3%;   Score 200.5; DB 7;   Length 159;
Best Local Similarity          35.2%;   Pred. No. 9.6e-11;
RESULT 918
ID    ABG96266 standard; protein; 221 AA.
DE    Human immunoglobulin superfamily protein IGSFP-4.
PN    WO200272794-A2.
PD    19-SEP-2002.
PA    (INCY-) INCYTE GENOMICS INC.
Query Match                    11.3%;   Score 199.5; DB 5;   Length 221;
Best Local Similarity          28.3%;   Pred. No. 1.9e-10;
RESULT 919
ID    ABM85690 standard; protein; 275 AA.
DE    Mouse protein sequence mCP1591.
PN    WO2003073826-A2.
PD    12-SEP-2003.
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PA (SAGR-) SAGRES DISCOVERY.
    Query Match   10.8%;   Score 190.5;   DB 7;   Length 275;
    Best Local Similarity 29.1%;
RESULT 920
ID AAR97632 standard; protein; 343 AA.
DE Mouse SLAM1 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
RESULT 921
    Query Match   10.5%;   Score 186;   DB 2;   Length 343;
    Best Local Similarity 24.3%;   Pred. No. 7.5e-09;
ID AAR97628 standard; protein; 335 AA.
DE Human SLAM1 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
RESULT 922
    Query Match   10.3%;   Score 182.5;   DB 2;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID AAB71853 standard; protein; 335 AA.
DE Human SLAM protein.
PN WO200111046-A1.
PD 15-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 923
    Query Match   10.3%;   Score 182.5;   DB 4;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID AAU11927 standard; protein; 335 AA.
DE Human protein sequence #1, related to isolation of genes within SLE-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA) UNIV TEXAS SYSTEM.
RESULT 924
    Query Match   10.3%;   Score 182.5;   DB 5;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID ABB90776 standard; protein; 335 AA.
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 285.
PN WO200210217-A2.
PD 07-FEB-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
RESULT 925
    Query Match   10.3%;   Score 182.5;   DB 5;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID ABU54483 standard; protein; 335 AA.
DE Human normal endothelial marker NEM 23.
PN WO200283874-A2.
PD 24-OCT-2002.
PA (UYJO) UNIV JOHNS HOPKINS.
RESULT 926
    Query Match   10.3%;   Score 182.5;   DB 6;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID ADL82887 standard; protein; 335 AA.
DE Human PRO12612, SEQ ID 89.
PN WO200424097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
RESULT 927
    Query Match   10.3%;   Score 182.5;   DB 8;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID ADP54607 standard; protein; 335 AA.
DE Human PRO protein sequence SEQ ID NO:583.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
RESULT 928
    Query Match   10.3%;   Score 182.5;   DB 8;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID ADY19726 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO 5532.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
RESULT 929
    Query Match   10.3%;   Score 182.5;   DB 9;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID ADY15680 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO 1486.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
RESULT 930
    Query Match   10.3%;   Score 182.5;   DB 9;   Length 335;
    Best Local Similarity 22.5%;   Pred. No. 1.6e-08;
ID AAG77978 standard; protein; 334 AA.
DE Human signalling lymphocytic activation molecule (SLAM)/SCZ.
PN WO200180717-A2.
PD 01-NOV-2001.
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
RESULT 931
    Query Match   10.2%;   Score 181.5;   DB 5;   Length 334;
    Best Local Similarity 22.6%;   Pred. No. 2e-08;
ID AAR97631 standard; protein; 307 AA.
DE Human SLAM4 T-cell co-stimulatory protein.
PN WO9617060-A1.
PD 06-JUN-1996.
PA (SCHE) SCHERING CORP.
RESULT 932
    Query Match   10.2%;   Score 180;   DB 2;   Length 307;
    Best Local Similarity 22.6%;   Pred. No. 2.4e-08;
ID AAY92181 standard; protein; 278 AA.
DE Murine TANGO 195.
PN WO200018800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
RESULT 933
    Query Match   10.1%;   Score 179;   DB 3;   Length 278;
    Best Local Similarity 25.9%;   Pred. No. 2.6e-08;
ID ABG74266 standard; protein; 278 AA.
DE Human transmembrane protein TANGO 195 form 2.
PN US2002155526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J.
RESULT 934
    Query Match   10.1%;   Score 179;   DB 6;   Length 278;
    Best Local Similarity 25.9%;   Pred. No. 2.6e-08;
ID ABW01426 standard; protein; 278 AA.
DE Murine TANGO 195 protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
RESULT 935
    Query Match   10.1%;   Score 179;   DB 7;   Length 278;
    Best Local Similarity 25.9%;   Pred. No. 2.6e-08;
ID ABW01428 standard; protein; 258 AA.
DE Murine TANGO 195 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
RESULT 936
    Query Match   10.0%;   Score 177.5;   DB 7;   Length 258;
    Best Local Similarity 27.0%;   Pred. No. 3.3e-09;
ID AAW67933 standard; protein; 33 AA.
DE Fragment of human secreted protein encoded by gene 5.
PN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 937
    Query Match   9.9%;   Score 175;   DB 2;   Length 33;
    Best Local Similarity 100.0%;   Pred. No. 2.9e-09;
ID ADS11838 standard; protein; 148 AA.
DE Human therapeutic contig protein - SEQ ID 2075.
PN WO200408148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
    Query Match   9.6%;   Score 170.5;   DB 8;   Length 148;

RESULT 938
ID   AAY43138 standard; protein; 365 AA.
DE   Human NAIL protein sequence.
PN   WO9950297-A1.
PD   07-OCT-1999.
PA   (IMMV-) IMMUNEX CORP.
Query Match   9.6%; Score 170; DB 2; Length 365;
Best Local Similarity   21.9%; Pred. No. 2.9e-07;

RESULT 939
ID   AAM23942 standard; protein; 365 AA.
DE   Human EST encoded protein SEQ ID NO:1467.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
Query Match   9.6%; Score 170; DB 4; Length 365;
Best Local Similarity   21.9%; Pred. No. 2.9e-07;

RESULT 940
ID   AAU11929 standard; protein; 365 AA.
DE   Human protein sequence #2, related to isolation of genes within SLE-1B.
PN   WO200188200-A2.
PD   22-NOV-2001.
PA   (TEXA) UNIV TEXAS SYSTEM.
Query Match   9.6%; Score 170; DB 5; Length 365;
Best Local Similarity   21.9%; Pred. No. 2.9e-07;

RESULT 941
ID   ADP56168 standard; protein; 365 AA.
DE   Human PRO protein sequence SEQ ID NO:2144.
PN   WO2004039956-A2.
PD   13-MAY-2004.
PA   (GETH) GENENTECH INC.
Query Match   9.6%; Score 170; DB 8; Length 365;
Best Local Similarity   21.9%; Pred. No. 2.9e-07;

RESULT 942
ID   ADP25183 standard; protein; 365 AA.
DE   PRO polypeptide SEQ ID NO:2361.
PN   WO2004041170-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
Query Match   9.6%; Score 170; DB 8; Length 365;
Best Local Similarity   21.9%; Pred. No. 2.9e-07;

RESULT 943
ID   AEF06406 standard; protein; 365 AA.
DE   Human CD244 NK cell receptor SEQ ID NO 24.
PN   WO2005085851-A2.
PD   15-SEP-2005.
PA   (ADRA/) ADRA C N.
Query Match   9.6%; Score 170; DB 10; Length 365;
Best Local Similarity   21.9%; Pred. No. 2.9e-07;

RESULT 944
ID   ABP41447 standard; protein; 391 AA.
DE   Human ovarian antigen HWACN71, SEQ ID NO:2579.
PN   WO200200677-A1.
PD   03-JAN-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   9.6%; Score 170; DB 5; Length 391;
Best Local Similarity   21.9%; Pred. No. 3.2e-07;

RESULT 945
ID   AAR97630 standard; protein; 305 AA.
DE   Human SLAM3 T-cell co-stimulatory protein.
PN   WO9617060-A1.
PD   06-JUN-1996.
PA   (SCHE) SCHERING CORP.
Query Match   9.3%; Score 164.5; DB 2; Length 305;
Best Local Similarity   21.7%; Pred. No. 7.7e-07;

RESULT 946
ID   ABB90777 standard; protein; 305 AA.
DE   Human Tumour Endothelial Marker polypeptide SEQ ID NO 286.
PN   WO200210217-A2.
PD   07-FEB-2002.
PA   (UYJO) UNIV JOHNS HOPKINS.
Query Match   9.3%; Score 164.5; DB 5; Length 305;
Best Local Similarity   21.7%; Pred. No. 7.7e-07;

RESULT 947
ID   ABU54484 standard; protein; 305 AA.
DE   Human normal endothelial marker NEM 23 secreted.
PN   WO200283874-A2.
PD   24-OCT-2002.
PA   (UYJO) UNIV JOHNS HOPKINS.
Query Match   9.3%; Score 164.5; DB 6; Length 305;
Best Local Similarity   21.7%; Pred. No. 7.7e-07;

RESULT 948
ID   AAR97633 standard; protein; 329 AA.
DE   Mouse SLAM2 T-cell co-stimulatory protein.
PN   WO9617060-A1.
PD   06-JUN-1996.
PA   (SCHE) SCHERING CORP.
Query Match   8.9%; Score 158.5; DB 2; Length 329;
Best Local Similarity   27.0%; Pred. No. 3.3e-06;

RESULT 949
ID   AAU11928 standard; protein; 329 AA.
DE   Mouse protein sequence #1, related to isolation of genes within SLE-1B.
PN   WO200188200-A2.
PD   22-NOV-2001.
PA   (TEXA) UNIV TEXAS SYSTEM.
Query Match   8.9%; Score 158.5; DB 5; Length 329;
Best Local Similarity   27.0%; Pred. No. 3.3e-06;

RESULT 950
ID   AAR97629 standard; protein; 298 AA.
DE   Human SLAM2 T-cell co-stimulatory protein.
PN   WO9617060-A1.
PD   06-JUN-1996.
PA   (SCHE) SCHERING CORP.
Query Match   8.6%; Score 152; DB 2; Length 298;
Best Local Similarity   23.4%; Pred. No. 1.2e-05;

RESULT 951
ID   ABB90778 standard; protein; 298 AA.
DE   Human Tumour Endothelial Marker polypeptide SEQ ID NO 287.
PN   WO200210217-A2.
PD   07-FEB-2002.
PA   (UYJO) UNIV JOHNS HOPKINS.
Query Match   8.6%; Score 152; DB 5; Length 298;
Best Local Similarity   23.4%; Pred. No. 1.2e-05;

RESULT 952
ID   ABU54485 standard; protein; 298 AA.
DE   Human normal endothelial marker NEM 23 short.
PN   WO200283874-A2.
PD   24-OCT-2002.
PA   (UYJO) UNIV JOHNS HOPKINS.
Query Match   8.6%; Score 152; DB 6; Length 298;
Best Local Similarity   23.4%; Pred. No. 1.2e-05;

RESULT 953
ID   AAY52479 standard; protein; 285 AA.
DE   Human D-SLAM.
PN   WO940184-A1.
PD   12-AUG-1999.
PA   (HELI-) HELIX RES INST.
Query Match   8.5%; Score 150.5; DB 3; Length 285;
Best Local Similarity   22.8%; Pred. No. 1.6e-05;

RESULT 954
ID   AAM93287 standard; protein; 285 AA.
DE   Human polypeptide, SEQ ID NO: 2773.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity   22.8%; Pred. No. 1.6e-05;

RESULT 955
ID   AAB71852 standard; protein; 285 AA.
DE   Human D-SLAM protein.
PN   WO200111046-A1.
PD   15-FEB-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity   22.8%; Pred. No. 1.6e-05;

RESULT 956

ID   AAB47323 standard; protein; 285 AA.
DE   APEX-3.
PN   WO200146260-A2.
PD   28-JUN-2001
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
     Query Match   8.5%;   Score 150.5;   DB 4;   Length 285
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 957
ID   AAE12075 standard; protein; 285 AA.
DE   Dendritic cell (DC) DCIGR protein.
PN   WO200172773-A2.
PD   04-OCT-2001.
PA   (NOVS) NOVARTIS AG.
PA   (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
     Query Match   8.5%;   Score 150.5;   DB 4;   Length 285
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 958
ID   ABG32412 standard; protein; 285 AA.
DE   Dendritic enriched secreted lymphocyte activation molecule (D-SLAM).
PN   WO200262955-A2.
PD   15-AUG-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   8.5%;   Score 150.5;   DB 5;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 959
ID   ADC78929 standard; protein; 285 AA.
DE   Human PRO protein #79.
PN   WO200304984-A2.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   8.5%;   Score 150.5;   DB 7;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 960
ID   ADD18914 standard; protein; 285 AA.
DE   Human disease related protein SeqID403.
PN   WO2003018621-A2.
PD   06-MAR-2003.
PA   (OXFO-) OXFORD BIOMEDICA UK LTD.
     Query Match   8.5%;   Score 150.5;   DB 7;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 961
ID   ADF15146 standard; protein; 285 AA.
DE   Human albumin fusion protein-related protein SeqID444.
PN   WO2003060071-A2.
PD   24-JUL-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (DELZ) DELTA BIOTECHNOLOGY LTD.
PA   (PRIN) PRINCIPIA PHARM CORP.
     Query Match   8.5%;   Score 150.5;   DB 7;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 962
ID   ADL30740 standard; protein; 285 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 2773.
PN   EP1395543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   8.5%;   Score 150.5;   DB 8;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 963
ID   ADQ21161 standard; protein; 285 AA.
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 3981.
PN   WO2004048938-A2.
PD   10-JUN-2004.
PA   (PROT-) PROTEIN DESIGN LABS INC.
     Query Match   8.5%;   Score 150.5;   DB 8;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 964
ID   ADR14157 standard; protein; 285 AA.
DE   Human NF-kappaB pathway-associated protein SeqID158.
PN   WO2004065577-A2.
PD   05-AUG-2004
PA   (BRIM) BRISTOL-MYERS SQUIBB CO.
     Query Match   8.5%;   Score 150.5;   DB 8;   Length 285;

Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 965
ID   ADP25075 standard; protein; 285 AA.
DE   PRO polypeptide SEQ ID NO:2253.
PN   WO200404170-A2.
PD   21-MAY-2004.
PA   (GETH) GENENTECH INC.
     Query Match   8.5%;   Score 150.5;   DB 8;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 966
ID   ADU06615 standard; protein; 285 AA.
DE   Novel bronchial cancer-associated human protein SeqID841.
PN   DE10316701-A1.
PD   04-NOV-2004.
PA   (HINZ/) HINZMANN B.
PA   (HERM/) HERMANN K.
PA   (CAST/) HEIDEN CASTANOS-VELEZ E.
     Query Match   8.5%;   Score 150.5;   DB 8;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 967
ID   ADY17598 standard; protein; 285 AA.
DE   PRO polypeptide SEQ ID NO 3404.
PN   WO200501696Z-A2.
PD   24-FEB-2005.
PA   (GETH) GENENTECH INC.
     Query Match   8.5%;   Score 150.5;   DB 9;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 968
ID   ADZ10066 standard; protein; 285 AA.
DE   Human breast cancer marker BLAME protein.
PN   EP1522594-A2.
PD   13-APR-2005.
PA   (FARB) BAYER HEALTHCARE AG.
     Query Match   8.5%;   Score 150.5;   DB 9;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 969
ID   AEK11565 standard; protein; 285 AA.
DE   Human slam family member 8 (SLAMF8), SEQ:82.
PN   US2006194238-A1.
PD   31-AUG-2006.
PA   (LATO/) LATOV N.
PA   (RENA/) RENAUD S.
     Query Match   8.5%;   Score 150.5;   DB 10;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 970
ID   AEJ92583 standard; protein; 285 AA.
DE   Human SLAM family member 8 (SLAMF8) protein.
PN   US2006194237-A1.
PD   31-AUG-2006.
PA   (LATO/) LATOV N.
PA   (RENA/) RENAUD S.
     Query Match   8.5%;   Score 150.5;   DB 10;   Length 285;
     Best Local Similarity 22.8%;   Pred. No. 1.6e-05;
RESULT 971
ID   ABW01429 standard; protein; 211 AA.
DE   Murine TANGO 195 protein extracellular domain.
PN   US2003113865-A1.
PD   19-JUN-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   8.3%;   Score 146.5;   DB 7;   Length 211;
     Best Local Similarity 28.6%;   Pred. No. 2.5e-05;
RESULT 972
ID   AAY92180 standard; protein; 312 AA.
DE   Partial human TANGO 195 protein.
PN   WO200018800-A1.
PD   06-APR-2000.
PA   (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
     Query Match   8.2%;   Score 146;   DB 3;   Length 312;
     Best Local Similarity 24.5%;   Pred. No. 4.9e-05;
RESULT 973
ID   ABG74265 standard; protein; 312 AA.
DE   Human transmembrane protein TANGO 195 form 1.
PN   US2002155526-A1.

PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J. 8.2%; Score 146; DB 6; Length 312;
Query Match 8.2%; Score 146; DB 6; Length 312;
Best Local Similarity 24.5%; Pred. No. 4.9e-05;
ID ABW01412 standard; protein; 312 AA.
DE Human TANGO 195 form 1 protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 146; DB 7; Length 312;
Best Local Similarity 24.5%; Pred. No. 4.9e-05;
ID AAM24013 standard; protein; 318 AA.
DE Human EST encoded protein SEQ ID NO: 1538.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.2%; Score 146; DB 4; Length 318;
Best Local Similarity 24.5%; Pred. No. 5.1e-05;
ID AAY92182 standard; protein; 320 AA.
DE Human partial TANGO 195 from clone T195Athpb93f1.
PN WO200018800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.2%; Score 146; DB 3; Length 320;
Best Local Similarity 24.5%; Pred. No. 5.1e-05;
ID ABG74267 standard; protein; 320 AA.
DE Human transmembrane protein TANGO 195, full length.
PN US2002155526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J. 8.2%; Score 146; DB 6; Length 320;
Query Match 8.2%; Score 146; DB 6; Length 320;
Best Local Similarity 24.5%; Pred. No. 5.1e-05;
ID ABW01436 standard; protein; 320 AA.
DE Human TANGO 195 form 2 protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 146; DB 7; Length 320;
Best Local Similarity 24.5%; Pred. No. 5.1e-05;
ID ADR10254 standard; protein; 211 AA.
DE Human protein useful for treating neurological disease Seq 3760.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.2%; Score 145; DB 8; Length 211;
Best Local Similarity 30.2%; Pred. No. 3.5e-05;
ID AAY92183 standard; protein; 285 AA.
DE Full-length human TANGO 195 protein.
PN WO200018800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.2%; Score 144.5; DB 3; Length 285;
Best Local Similarity 22.5%; Pred. No. 6.1e-05;
ID ABG74268 standard; protein; 285 AA.
DE Mouse transmembrane protein TANGO 195.
PN US2002155526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J. 8.2%; Score 144.5; DB 6; Length 285;
Query Match 8.2%; Score 144.5; DB 6; Length 285;
Best Local Similarity 22.5%; Pred. No. 6.1e-05;
ID ABW01442 standard; protein; 285 AA.
DE Human TANGO 195 protein.
PN US2003113865-A1.
PD 19-JUN-2003.

PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 144.5; DB 7; Length 285;
Best Local Similarity 22.5%; Pred. No. 6.1e-05;
ID ADZ13290 standard; protein; 344 AA.
DE Murine cancer-associated protein #90.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR) CHIRON CORP.
Query Match 8.1%; Score 144; DB 9; Length 344;
Best Local Similarity 21.4%; Pred. No. 8.9e-05;
ID ABM85810 standard; protein; 358 AA.
DE Mouse protein sequence mCP3002.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 8.1%; Score 144; DB 7; Length 358;
Best Local Similarity 21.4%; Pred. No. 9.5e-05;
ID ABG75379 standard; protein; 416 AA.
DE Predicted INSP052 protein.
PN WO2003093316-A2.
PD 13-NOV-2003.
PA (ARES-) ARES TRADING SA.
Query Match 8.0%; Score 142.5; DB 7; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00016;
ID ABG75377 standard; protein; 416 AA.
DE Human INSP052 complete protein.
PN WO2003093316-A2.
PD 13-NOV-2003.
PA (ARES-) ARES TRADING SA.
Query Match 8.0%; Score 142.5; DB 7; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00016;
ID ADO47892 standard; protein; 416 AA.
DE Human protein SEQ ID NO:9.
PN WO2004007672-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 8.0%; Score 142.5; DB 8; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00016;
ID ADS11056 standard; protein; 416 AA.
DE Human therapeutic protein - SEQ ID 1293.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 8.0%; Score 142.5; DB 8; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00016;
ID AEA27921 standard; protein; 416 AA.
DE Cell surface recognition molecule INSP052.
PN WO2005046714-A2.
PD 26-MAY-2005.
PA (ARES-) ARES TRADING SA.
Query Match 8.0%; Score 142.5; DB 9; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00016;
ID ADQ65357 standard; protein; 367 AA.
DE Novel human protein sequence #330.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.0%; Score 142; DB 8; Length 367;
Best Local Similarity 22.2%; Pred. No. 0.00015;
ID ADA07622 standard; peptide; 149 AA.
DE Human secreted protein from gene 43, peptide #2.
PN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.

RESULT 974
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RESULT 976
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RESULT 991

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PA    (ROSE/) ROSEN C A.
PA    (SOPP/) SOPPET D R.
PA    (RUBE/) RUBEN S M.
PA    (KYAW/) KYAW H.
PA    (LIYY/) LI Y.
PA    (ZENG/) ZENG Z.
PA    (LAFL/) LAFLEUR D W.
PA    (MOOR/) MOORE P A.
PA    (SHIY/) SHI Y.
PA    (OLSE/) OLSEN H S.
PA    (EBNE/) EBNER R.
PA    (BREW/) BREWER L A.
      Query Match          8.0%;   Score 141; DB 7; Length 149;
      Best Local Similarity 30.7%;  Pred. No. 5.1e-05;
RESULT 993
ID    ADN41449 standard; protein; 149 AA.
DE    Novel human secreted protein fragment seqid 571.
PN    US200404191-A1.
PD    04-MAR-2004.
PA    (FISC/) FISCHER C L.
PA    (ROSE/) ROSEN C A.
PA    (SOPP/) SOPPET D R.
PA    (RUBE/) RUBEN S M.
PA    (KYAW/) KYAW H.
PA    (LIYY/) LI Y.
PA    (ZENG/) ZENG Z.
PA    (LAFL/) LAFLEUR D W.
PA    (MOOR/) MOORE P A.
PA    (SHIY/) SHI Y.
PA    (OLSE/) OLSEN H.
PA    (EBNE/) EBNER R.
PA    (BIRS/) BIRSE C E.
      Query Match          8.0%;   Score 141; DB 8; Length 149;
      Best Local Similarity 30.7%;  Pred. No. 5.1e-05;
RESULT 994
ID    ADA57556 standard; protein; 142 AA.
DE    Human secreted protein #504.
PN    WO2002102994-A2.
PD    27-DEC-2002.
PA    (HUMA-) HUMAN GENOME SCI INC.
      Query Match          7.9%;   Score 140.5; DB 6; Length 142;
      Best Local Similarity 31.0%;  Pred. No. 5.3e-05;
RESULT 995
ID    ADA41448 standard; protein; 142 AA.
DE    Human secreted protein.
PN    WO2002102993-A2.
PD    27-DEC-2002.
PA    (HUMA-) HUMAN GENOME SCI INC.
      Query Match          7.9%;   Score 140.5; DB 6; Length 142;
      Best Local Similarity 31.0%;  Pred. No. 5.3e-05;
RESULT 996
ID    ADC74567 standard; protein; 142 AA.
DE    Human secreted protein - SEQ ID 1200.
PN    WO2003038063-A2.
PD    08-MAY-2003.
PA    (HUMA-) HUMAN GENOME SCI INC.
      Query Match          7.9%;   Score 140.5; DB 7; Length 142;
      Best Local Similarity 31.0%;  Pred. No. 5.3e-05;
RESULT 997
ID    ADN41130 standard; protein; 142 AA.
DE    Novel human secreted protein seqid 252.
PN    US200404191-A1.
PD    04-MAR-2004.
PA    (FISC/) FISCHER C L.
PA    (ROSE/) ROSEN C A.
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PA    (SOPP/) SOPPET D R.
PA    (RUBE/) RUBEN S M.
PA    (KYAW/) KYAW H.
PA    (LIYY/) LI Y.
PA    (ZENG/) ZENG Z.
PA    (LAFL/) LAFLEUR D W.
PA    (MOOR/) MOORE P A.
PA    (SHIY/) SHI Y.
PA    (OLSE/) OLSEN H.
PA    (EBNE/) EBNER R.
PA    (BIRS/) BIRSE C E.
      Query Match          7.9%;   Score 140.5; DB 8; Length 142;
      Best Local Similarity 31.0%;  Pred. No. 5.3e-05;
RESULT 998
ID    AEL02398 standard; protein; 142 AA.
DE    Human secreted protein amino acid sequence - SEQ ID 576.
PN    US2006223090-A1.
PD    05-OCT-2006.
      Query Match          7.9%;   Score 140.5; DB 10; Length 142;
      Best Local Similarity 31.0%;  Pred. No. 5.3e-05;
RESULT 999
ID    AEL29769 standard; protein; 142 AA.
DE    Human secreted protein, SEQ ID 1749.
PN    US2006223088-A1.
PD    05-OCT-2006.
      Query Match          7.9%;   Score 140.5; DB 10; Length 142;
      Best Local Similarity 31.0%;  Pred. No. 5.3e-05;
RESULT 1000
ID    AAY02692 standard; protein; 143 AA.
DE    Human secreted protein encoded by gene 43 clone HTADX17.
PN    WO9902546-A1.
PD    21-JAN-1999.
PA    (HUMA-) HUMAN GENOME SCI INC.
      Query Match          7.9%;   Score 140.5; DB 2; Length 143;
      Best Local Similarity 31.0%;  Pred. No. 5.4e-05;
RESULT 1001
ID    ADA07371 standard; protein; 143 AA.
DE    Human secreted protein from gene 43.
PN    US2003064412-A1.
PD    03-APR-2003.
PA    (FISC/) FISCHER C L.
PA    (ROSE/) ROSEN C A.
PA    (SOPP/) SOPPET D R.
PA    (RUBE/) RUBEN S M.
PA    (KYAW/) KYAW H.
PA    (LIYY/) LI Y.
PA    (ZENG/) ZENG Z.
PA    (LAFL/) LAFLEUR D W.
PA    (MOOR/) MOORE P A.
PA    (SHIY/) SHI Y.
PA    (OLSE/) OLSEN H S.
PA    (EBNE/) EBNER R.
PA    (BREW/) BREWER L A.
      Query Match          7.9%;   Score 140.5; DB 7; Length 143;
      Best Local Similarity 31.0%;  Pred. No. 5.4e-05;
RESULT 1002
ID    ABW01419 standard; protein; 290 AA.
DE    Human TANGO 195 form 1 mature protein.
PN    US2003113865-A1.
PD    19-JUN-2003.
PA    (MILL-) MILLENNIUM PHARM INC.
      Query Match          7.9%;   Score 140.5; DB 7; Length 290;
      Best Local Similarity 28.0%;  Pred. No. 0.00015;
RESULT 1003
ID    ABW01438 standard; protein; 298 AA.
DE    Human TANGO 195 form 2 mature protein.
PN    US2003113865-A1.
PD    19-JUN-2003.
PA    (MILL-) MILLENNIUM PHARM INC.
      Query Match          7.9%;   Score 140.5; DB 7; Length 298;
      Best Local Similarity 28.0%;  Pred. No. 0.00016;
RESULT 1004
ID    AAW67932 standard; protein; 28 AA.
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DE   Fragment of human secreted protein encoded by gene 5.
PN   WO9842738-A1.
PD   01-OCT-1998.
PA   (HUMA-) HUMAN GENOME SCI INC.
     Query Match   7.8%; Score 139; DB 2; Length 28;
     Best Local Similarity   100.0%; Pred. No. 6.9e-06;
RESULT 1005
ID   ABW01444 standard; protein; 263 AA.
DE   Human TANGO 195 mature protein.
PN   US2003113865-A1.
PD   19-JUN-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   7.8%; Score 139; DB 7; Length 263;
     Best Local Similarity   24.3%; Pred. No. 0.00018;
RESULT 1006
ID   ABG75378 standard; protein; 418 AA.
DE   Murine INSP052 complete protein.
PN   WO2003093316-A2.
PD   13-NOV-2003.
PA   (ARES-) ARES TRADING SA.
     Query Match   7.8%; Score 138.5; DB 7; Length 418;
     Best Local Similarity   22.9%; Pred. No. 0.00041;
RESULT 1007
ID   AEA27923 standard; protein; 418 AA.
DE   Cell surface recognition molecule INSP055.
PN   WO2005046714-A2.
PD   26-MAY-2005.
PA   (ARES-) ARES TRADING SA.
     Query Match   7.8%; Score 138.5; DB 9; Length 418;
     Best Local Similarity   22.9%; Pred. No. 0.00041;
RESULT 1008
ID   AAE26255 standard; protein; 70 AA.
DE   Human CD2001 protein Ig domain.
PN   EP1223218-A1.
PD   17-JUL-2002.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   7.8%; Score 138; DB 5; Length 70;
     Best Local Similarity   32.9%; Pred. No. 3.3e-05;
RESULT 1009
ID   ABW01835 standard; protein; 70 AA.
DE   Human CD2001 protein immunoglobulin (Ig) domain.
PN   US2003180888-A1.
PD   25-SEP-2003.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   7.8%; Score 138; DB 7; Length 70;
     Best Local Similarity   32.9%; Pred. No. 3.3e-05;
RESULT 1010
ID   ADO47895 standard; protein; 383 AA.
DE   Human mature protein SEQ ID NO:12.
PN   WO2004007672-A2.
PD   22-JAN-2004.
PA   (NUVE-) NUVELO INC.
     Query Match   7.8%; Score 137.5; DB 8; Length 383;
     Best Local Similarity   22.0%; Pred. No. 0.00045;
RESULT 1011
ID   AEA27931 standard; protein; 383 AA.
DE   Human INSP052 mature polypeptide.
PN   WO2005046714-A2.
PD   26-MAY-2005.
PA   (ARES-) ARES TRADING SA.
     Query Match   7.8%; Score 137.5; DB 9; Length 383;
     Best Local Similarity   22.0%; Pred. No. 0.00045;
RESULT 1012
ID   ADM72195 standard; protein; 327 AA.
DE   Human CD2 amino acid sequence.
PN   WO2004022097-A1.
PD   18-MAR-2004.
PA   (MEDI-) MEDIMMUNE INC.
     (USSH) US NAT CANCER INST.
     Query Match   7.8%; Score 136.5; DB 8; Length 327;
     Best Local Similarity   23.9%; Pred. No. 0.00044;
RESULT 1013
ID   AAY83135 standard; protein; 351 AA.

DE   Human CD2.
PN   WO200012113-A2.
PD   09-MAR-2000.
PA   (BIOJ) BIOGEN INC.
     Query Match   7.8%; Score 136.5; DB 3; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1014
ID   AAB61159 standard; protein; 351 AA.
DE   Human CD2.
PN   US6162432-A.
PD   19-DEC-2000.
PA   (UNMI) UNIV MICHIGAN.
PA   (BIOJ) BIOGEN INC.
     Query Match   7.8%; Score 136.5; DB 4; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1015
ID   ABB81993 standard; protein; 351 AA.
DE   Human CD2 polypeptide.
PN   WO20026048O-A1.
PD   08-AUG-2002.
PA   (BIOJ) BIOGEN INC.
     Query Match   7.8%; Score 136.5; DB 5; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1016
ID   AAU76227 standard; protein; 351 AA.
DE   Mammalian CD2 antigen protein.
PN   US2002009449-A1.
PD   24-JAN-2002.
PA   (BIOJ) BIOGEN INC.
     Query Match   7.8%; Score 136.5; DB 5; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1017
ID   ABM85811 standard; protein; 351 AA.
DE   Human protein sequence hCP48906.
PN   WO2003073826-A2.
PD   12-SEP-2003.
PA   (SAGR-) SAGRES DISCOVERY.
     Query Match   7.8%; Score 136.5; DB 7; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1018
ID   ADQ60208 standard; protein; 351 AA.
DE   Human CD2 protein.
PN   US2004136987-A1.
PD   15-JUL-2004.
PA   (BIOJ) BIOGEN INC.
     (UNMI) UNIV MICHIGAN.
     Query Match   7.8%; Score 136.5; DB 8; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1019
ID   ADZ13293 standard; protein; 351 AA.
DE   Human cancer-associated protein #249.
PN   WO2005031001-A2.
PD   07-APR-2005.
PA   (CHIR) CHIRON CORP.
     Query Match   7.8%; Score 136.5; DB 9; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1020
ID   AEG93652 standard; protein; 351 AA.
DE   Human T-lymphocyte surface glycoprotein CD2 (T11).
PN   US2006084107-A1.
PD   20-APR-2006.
PA   (WALL/) WALLNER B P.
     (COOP/) COOPER K D.
     Query Match   7.8%; Score 136.5; DB 10; Length 351;
     Best Local Similarity   23.9%; Pred. No. 0.00049;
RESULT 1021
ID   AAR06365 standard; protein; 353 AA.
DE   Soluble two domain human CD2 glycoprotein.
PN   WO9008187-A.
PD   26-JUL-1990.
PA   (DAND) DANA FARBER CANCER INST INC.
     Query Match   7.8%; Score 136.5; DB 2; Length 353;
     Best Local Similarity   23.9%; Pred. No. 0.00049;

RESULT 1022
ID   AEH89917 standard; protein; 289 AA.
DE   Mouse calcineurin-regulated kringle domain (CRKD) protein SEQ ID: 6.
PN   US2006110395-A1.
PD   25-MAY-2006.
PA   (CRAB/) CRABTREE G R.
PA   (CORB/) CORBIT K.
     Query Match   7.6%;   Score 135.5; DB 10; Length 289;
     Best Local Similarity   21.4%;   Pred. No. 0.00046;
RESULT 1023
ID   AEK49158 standard; peptide; 23 AA.
DE   EGFR-related phosphorylation site peptide sequence, SEQ ID NO:97.
PN   WO2006068640-A1.
PD   29-JUN-2006.
PA   (CELL-) CELL SIGNALING TECHNOLOGY INC.
     Query Match   100.0%;   Score 135; DB 10; Length 23;
     Best Local Similarity   100.0%;   Pred. No. 1.3e-05;
RESULT 1024
ID   AAU29274 standard; protein; 198 AA.
DE   Human PRO polypeptide sequence #251.
PN   WO200168848-A2.
PD   20-SEP-2001.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5; DB 4; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1025
ID   ABU58650 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003027272-A1.
PD   06-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1026
ID   ABU88198 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003032127-A1.
PD   13-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1027
ID   ABU84513 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032112-A1.
PD   13-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1028
ID   ABR66387 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027278-A1.
PD   06-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1029
ID   ABR65777 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036159-A1.
PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1030
ID   ABU99717 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040070-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1031
ID   ABU82956 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003032113-A1.
PD   13-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;

     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1032
ID   ABU90077 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003036147-A1.
PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1033
ID   ABR68326 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027264-A1.
PD   06-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1034
ID   ABU96379 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003036144-A1.
PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1035
ID   ABU92810 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036149-A1.
PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1036
ID   ABO08887 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003044923-A1.
PD   06-MAR-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1037
ID   ABO02939 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040062-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1038
ID   ABR75093 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040056-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1039
ID   ABR94855 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003044926-A1.
PD   06-MAR-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1040
ID   ABU85828 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003036140-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1041
ID   ABU98988 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003013153-A1.
PD   16-JAN-2003.
     Query Match   7.6%;   Score 134.5; DB 6; Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1042

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ID   ABU98203 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003017544-A1.
PD   23-JAN-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1043
ID   ABU91909 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003027277-A1.
PD   06-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1044
ID   ABU89602 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003036141-A1.
PD   20-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1045
ID   ABU86443 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036146-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1046
ID   ABU67656 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036162-A1.
PD   20-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1047
ID   ABU80684 standard; protein; 198 AA.
DE   Human PRO protein #251.
PN   US2003036137-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1048
ID   ABR99602 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040063-A1.
PD   27-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1049
ID   ABR98992 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040064-A1.
PD   27-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1050
ID   ABO16515 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003022267-A1.
PD   06-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1051
ID   ABR92415 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036160-A1.
PD   20-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1052

ID   ABO19056 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003044925-A1.
PD   06-MAR-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1053
ID   ABR78477 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054474-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1054
ID   ABU85213 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003032114-A1.
PD   13-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1055
ID   ABO00352 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003032101-A1.
PD   13-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1056
ID   ABO11684 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040054-A1.
PD   27-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1057
ID   ABO02329 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040054-A1.
PD   27-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1058
ID   ABU88903 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003036133-A1.
PD   20-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1059
ID   ABU83598 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036134-A1.
PD   20-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1060
ID   ABO06399 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003022294-A1.
PD   30-JAN-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1061
ID   ABR59435 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027275-A1.
PD   06-FEB-2003.
     Query Match             7.6%;  Score 134.5;  DB 6;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1062
ID   ABO09497 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
```

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PN   US2003027324-A1.
PD   06-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
ID   AB019361 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003036118-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1064
ID   AB011379 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036123-A1.
PD   20-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1065
ID   ABR66997 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036148-A1.
PD   20-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1066
ID   AB016210 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040060-A1.
PD   27-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1067
ID   AB013916 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003044916-A1.
PD   06-MAR-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1068
ID   ABU65819 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein, SEQ ID 502.
PN   US2003036156-A1.
PD   20-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1069
ID   AB007667 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003032117-A1.
PD   13-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1070
ID   AB003854 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036128-A1.
PD   20-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1071
ID   ABR67302 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027266-A1.
PD   06-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1072
ID   AB015905 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003054483-A1.
PD   20-MAR-2003.


PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1073
ID   ABU56186 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein, PRO4421.
PN   US2003022298-A1.
PD   30-JAN-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1074
ID   ABU65514 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003032102-A1.
PD   13-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1075
ID   ABU95459 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421
PN   US2003036117-A1.
PD   20-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1076
ID   ABU71362 standard; protein; 198 AA.
DE   Human PRO4421 protein.
PN   US2003036143-A1.
PD   20-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1077
ID   AB007972 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003032130-A1.
PD   13-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1078
ID   ABR70213 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003032138-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1079
ID   ABR69546 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036132-A1.
PD   20-FEB-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1080
ID   AB001687 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003008353-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1081
ID   ABU81489 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003017542-A1.
PD   23-JAN-2003.
     Query Match        7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1082
ID   ABR60286 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003032137-A1.
PD   13-FEB-2003.
```

RESULT 1083
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABR68021 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027269-A1.
PD   06-FEB-2003.
```

RESULT 1084
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABR65409 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027268-A1.
PD   06-FEB-2003.
```

RESULT 1085
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABR68631 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027274-A1.
PD   06-FEB-2003.
```

RESULT 1086
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABR72043 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003032135-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
```

RESULT 1087
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABU85523 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003022295-A1.
PD   30-JAN-2003.
```

RESULT 1088
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABU89213 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003022297-A1.
PD   30-JAN-2003.
```

RESULT 1089
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABU83293 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032105-A1.
PD   13-FEB-2003.
```

RESULT 1090
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABU95149 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003032123-A1.
PD   13-FEB-2003.
```

RESULT 1091
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABU90697 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003032108-A1.
PD   13-FEB-2003.
```

RESULT 1092
```
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
ID   ABU84208 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032111-A1.
PD   13-FEB-2003.
```

RESULT 1093
```
ID   ABU93859 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003032119-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1094
```
ID   ABR65104 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027263-A1.
PD   06-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1095
```
ID   ABR68936 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027271-A1.
PD   06-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1096
```
ID   AB006752 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036125-A1.
PD   20-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1097
```
ID   ABR99297 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040068-A1.
PD   27-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1098
```
ID   ABU57181 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003027280-A1.
PD   06-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1099
```
ID   ABU86133 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003022300-A1.
PD   30-JAN-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1100
```
ID   ABU82420 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003036136-A1.
PD   20-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1101
```
ID   ABU87431 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003036138-A1.
PD   20-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1102
```
ID   ABU93903 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032109-A1.
PD   13-FEB-2003.
Query Match      Best Local Similarity   7.6%;   Score 134.5; DB 6;   Length 198;
                                        30.7%;   Pred. No. 0.00033;
```

RESULT 1103
```
ID   AB008277 standard; protein; 198 AA.
```

```
DE  Human PRO polypeptide #251.
PN  US2003040066-A1.
PD  27-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1104
ID  ABU81988 standard; protein; 198 AA.
DE  Novel human secreted and transmembrane protein PRO4421.
PN  US2003032104-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1105
ID  ABU66152 standard; protein; 198 AA.
DE  Novel human secreted and transmembrane protein PRO4421.
PN  US2003036157-A1.
PD  20-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1106
ID  ABR59981 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003032120-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1107
ID  ABU94169 standard; protein; 198 AA.
DE  Novel human secreted and transmembrane protein PRO4421.
PN  US2003036155-A1.
PD  20-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1108
ID  ABO00042 standard; protein; 198 AA.
DE  Novel human secreted and transmembrane protein PRO4421.
PN  US2003022296-A1.
PD  30-JAN-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1109
ID  ABR66692 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003027281-A1.
PD  06-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1110
ID  ABR91110 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003040058-A1.
PD  27-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1111
ID  ABU94537 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003017540-A1.
PD  23-JAN-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1112
ID  ABU79419 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003032106-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1113
ID  ABU86748 standard; protein; 198 AA.
DE  Human secreted/transmembrane protein (PRO) #251.
PN  US2003032129-A1.

PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1114
ID  ABU87053 standard; protein; 198 AA.
DE  Novel human secreted and transmembrane protein PRO4421.
PN  US2003032131-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1115
ID  ABU94842 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003032103-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1116
ID  ABO04769 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003032107-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1117
ID  ABR70518 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003032139-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1118
ID  ABU98683 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003022301-A1.
PD  30-JAN-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1119
ID  ABR66082 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003036165-A1.
PD  20-FEB-2003.
PA  (GETH ) GENENTECH INC.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1120
ID  ABR64799 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003027262-A1.
PD  06-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1121
ID  ABU79724 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003032110-A1.
PD  13-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1122
ID  ABU93115 standard; protein; 198 AA.
DE  Human secreted/transmembrane protein (PRO) #251.
PN  US2003036142-A1.
PD  20-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
    Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1123
ID  ABU96074 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003036145-A1.
PD  20-FEB-2003.
    Query Match    7.6%;   Score 134.5;   DB 6;   Length 198;
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Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1124
ID   ABU91294 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003036154-A1.
PD   20-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1125
ID   ABU90387 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003036153-A1.
PD   20-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1126
ID   ABO09802 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003044931-A1.
PD   06-MAR-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1127
ID   ABO11074 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036150-A1.
PD   20-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1128
ID   ABR71128 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040069-A1.
PD   27-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1129
ID   ABU87736 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003022293-A1.
PD   30-JAN-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1130
ID   ABU91604 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003032128-A1.
PD   13-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1131
ID   ABU84818 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032116-A1.
PD   13-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1132
ID   ABR69908 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003122122-A1.
PD   13-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1133
ID   ABU80285 standard; protein; 198 AA.
DE   Human PRO protein #251.
PN   US2003036139-A1.
PD   20-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1134
ID   ABU93554 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003017541-A1.
PD   23-JAN-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1135
ID   ABO10107 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003017543-A1.
PD   23-JAN-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1136
ID   ABO09192 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036152-A1.
PD   20-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1137
ID   ABU10760 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein #251.
PN   US2002127584-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1138
ID   ABU95769 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003032115-A1.
PD   13-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1139
ID   ABU96978 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003032140-A1.
PD   13-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1140
ID   ABR70823 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040076-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1141
ID   ABO08582 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003044922-A1.
PD   09-JAN-2003.
PA   (GETH ) GENENTECH INC.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1142
ID   ABO05174 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003008352-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1143
ID   ABO05789 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032118-A1.
PD   13-FEB-2003.
Query Match                    7.6%;   Score 134.5;   DB 6;   Length 198;
Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1144
ID   ABR74178 standard; protein; 198 AA.
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DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003036135-A1.
PD  20-FEB-2003.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1145
ID  ABR95770 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003054455-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1146
ID  ABR81067 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003049741-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1147
ID  ABR81372 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003049743-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1148
ID  ABM01068 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003049769-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1149
ID  ABR88670 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003068743-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1150
ID  ABM77491 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003054479-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1151
ID  ABO28975 standard; protein; 198 AA.
DE  Human secreted/transmembrane protein (PRO) #251.
PN  US2003068685-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1152
ID  ABO31720 standard; protein; 198 AA.
DE  Human secreted/transmembrane protein (PRO) #251.
PN  US2003068725-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1153
ID  ABM08137 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003068752-A1.

PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1154
ID  ABO40617 standard; protein; 198 AA.
DE  Human secreted/transmembrane protein (PRO) #251.
PN  US2003068682-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1155
ID  ABO36042 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003068701-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1156
ID  ABO44181 standard; protein; 198 AA.
DE  Human PRO polypeptide #251.
PN  US2003068755-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1157
ID  ADA78254 standard; protein; 198 AA.
DE  Human secreted/transmembrane protein (PRO) #251.
PN  US2003073180-A1.
PD  17-APR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1158
ID  ABM24976 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003104533-A1.
PD  05-JUN-2003.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1159
ID  ABO03244 standard; protein; 198 AA.
DE  Human secreted/transmembrane protein (PRO) #251.
PN  US2003036131-A1.
PD  20-FEB-2003.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1160
ID  ABR90500 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003040075-A1.
PD  27-FEB-2003.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1161
ID  ABM17414 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003054459-A1.
PD  20-MAR-2003.
PA  (GETH ) GENENTECH INC.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1162
ID  ABR95160 standard; protein; 198 AA.
DE  Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN  US2003044930-A1.
PD  06-MAR-2003.
    Query Match        7.6%;  Score 134.5;  DB 6;  Length 198;
    Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1163
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ID   ABR95465 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040071-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1164
ID   ABO21703 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003054471-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1165
ID   ABR97967 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064452-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1166
ID   ABR87755 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068705-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1167
ID   ABM77796 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054473-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1168
ID   ABM28026 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064440-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1169
ID   ABM06307 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068704-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1170
ID   ABM03813 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068722-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1171
ID   ABM35264 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073183-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1172
ID   ABM26501 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN   US2003104549-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1173
ID   ABO48283 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049749-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1174
ID   ABR93025 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064462-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1175
ID   ABO24786 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003065159-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1176
ID   ABM11797 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064447-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1177
ID   ABM02898 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073184-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1178
ID   ABM16194 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064463-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1179
ID   ABO27755 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1180
ID   ABM29246 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068721-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match            7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1181
ID   ABM07222 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068699-A1.
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PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1182
ID   ABM21316 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068707-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1183
ID   ABM09662 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073175-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1184
ID   ABO41532 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068695-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1185
ID   ABO36347 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003068703-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1186
ID   ABO43876 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003068732-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1187
ID   ABM76576 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003082717-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1188
ID   ABM76272 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104548-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1189
ID   ABM25891 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104542-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1190
ID   ABM26196 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104543-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;

RESULT 1191
ID   ABO03549 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036127-A1.
PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1192
ID   ABO02634 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040061-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1193
ID   ABR90805 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036130-A1.
PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1194
ID   ABR73873 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054468-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1195
ID   ABO17125 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003054470-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1196
ID   ABR94550 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003044917-A1.
PD   06-MAR-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1197
ID   ABR76057 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003044929-A1.
PD   06-MAR-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1198
ID   ABR71433 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003059880-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1199
ID   ABR93330 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064465-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1200
ID   ABR93635 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054478-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.

RESULT 1201
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABR88060 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1202
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO28060 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1203
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO30195 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1204
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO33404 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1205
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABM05092 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1206
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABM09052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1207
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO35737 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1208
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO39702 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1209
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABM10577 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1210
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABM12102 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 1211
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO52248 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1212
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO52553 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1213
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABO23871 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
RESULT 1214
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABR97357 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1215
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABR87145 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1216
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABM11187 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1217
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
ID ABM28331 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1218
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1219
Query Match 7.6%; Score 134.5; DB 6; Length 198;

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ID   ABO32330 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068733-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1220
ID   ABM15457 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068692-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1221
ID   ABM06612 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068709-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1222
ID   ABM04423 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068716-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1223
ID   ABM22536 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068740-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1224
ID   ABM07832 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068751-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1225
ID   ABO40922 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068684-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1226
ID   ABM35569 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073179-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1227
ID   ABM33332 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003087374-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1228
ID   ABO52858 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.

PN   US2003049773-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1229
ID   ABO50418 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049777-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1230
ID   ABU99412 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040055-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1231
ID   ABO04464 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036164-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1232
ID   ABM18634 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054480-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1233
ID   ABR97662 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003059885-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1234
ID   ABR80762 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049740-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1235
ID   ABM01373 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049770-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1236
ID   ABR88975 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073169-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;
RESULT 1237
ID   ABM13627 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064457-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match          7.6%;   Score 134.5;  DB 6;   Length 198;
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        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1238
ID   ABM21011 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068711-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1239
ID   ABO42142 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049945-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1240
ID   ABO42752 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049751-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1241
ID   ABM10272 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003067478-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1242
ID   ABO38787 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068773-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1243
ID   ABM33027 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073185-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1244
ID   ABM22841 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003087373-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1245
ID   ABM75052 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003096353-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1246
ID   ADA80046 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073173-A1.
PD   17-APR-2003.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1247
ID   ABR96442 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
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PN   US200305454S8-A1.
PD   20-MAR-2003.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1248
ID   ABM02593 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003059886-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1249
ID   ABR86535 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049758-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1250
ID   ABR86840 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049772-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1251
ID   ABM16804 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1252
ID   ABM29856 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1253
ID   ABO29280 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1254
ID   ABM24061 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1255
ID   ABM23451 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
        Query Match         7.6%;  Score 134.5;  DB 6;  Length 198;
        Best Local Similarity  30.7%;  Pred. No. 0.00033;
RESULT 1256
ID   ABM22231 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068742-A1.
PD   10-APR-2003.
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PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1257
ID ABO37872 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1258
ID ABM28636 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082716-A1.
PD 01-MAY-2003.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1259
ID ABM28941 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082716-A1.
PD 01-MAY-2003.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1260
ID ABM66585 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1261
ID ABM75967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1262
ID ABM34247 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1263
ID ABM34552 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1264
ID ABO20483 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1265
ID ABO21398 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054454-A1.
PD 20-MAR-2003.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1266
ID ABO22313 standard; protein; 198 AA.

DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1267
ID ABR96747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1268
ID ABR85925 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1269
ID ABR99907 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1270
ID ABM00458 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1271
ID ABM00763 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073172-A1.
PD 17-APR-2003.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1272
ID ABO29890 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1273
ID ABM23756 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1274
ID ABM29551 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 134.5; DB 6; Length 198;
  Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1275
ID ABO38482 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068767-A1.
PD 10-APR-2003.

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PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1276
ID   ABO45782 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003073182-A1.
PD   17-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1277
ID   ABM20706 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104557-A1.
PD   05-JUN-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1278
ID   ADA81773 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003092121-A1.
PD   15-MAY-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1279
ID   ABO16820 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003027276-A1.
PD   06-FEB-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1280
ID   ABO18446 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003044920-A1.
PD   06-MAR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1281
ID   ABO22873 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003027265-A1.
PD   06-FEB-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1282
ID   ABO23178 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003054461-A1.
PD   20-MAR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1283
ID   ABR92720 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064446-A1.
PD   03-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1284
ID   ABR81677 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049744-A1.
PD   13-MAR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1285

ID   ABM78101 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049783-A1.
PD   13-MAR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1286
ID   ABR89890 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073171-A1.
PD   17-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1287
ID   ABM28806 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003032121-A1.
PD   13-FEB-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1288
ID   ABM13932 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064458-A1.
PD   03-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1289
ID   ABO28670 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003064460-A1.
PD   03-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1290
ID   ABO30500 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003064464-A1.
PD   03-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1291
ID   ABM07527 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068702-A1.
PD   10-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1292
ID   ABM04118 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068734-A1.
PD   10-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1293
ID   ABO37262 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068719-A1.
PD   10-APR-2003.
PA    (GETH ) GENENTECH INC.
   Query Match                    7.6%;    Score 134.5; DB 6;  Length 198;
   Best Local Similarity   30.7%;  Pred. No. 0.00033;
RESULT 1294
ID   ABO41837 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068729-A1.
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PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1295
ID ABO35432 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1296
ID ABM25281 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1297
ID ABO47673 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1298
ID ABO47978 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049747-A1.
PD 13-MAR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1299
ID ABO48588 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1300
ID ABO51638 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1301
ID ABO51943 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1302
ID ABO50723 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1303
ID ABR79847 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1304
ID ABM17109 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1305
ID ABO18141 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1306
ID ABO21093 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1307
ID ABR97052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1308
ID ABM12407 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1309
ID ABM16499 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1310
ID ABM24366 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1311
ID ABM14847 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1312
ID ABM04728 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1313
ID ABM06917 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN   US2003068730-A1
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1314
ID   ABM09357 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073174-A1.
PD   17-APR-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1315
ID   ABO39397 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068775-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1316
ID   ABM75662 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104545-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1317
ID   ABM25586 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104541-A1.
PD   05-JUN-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1318
ID   ABM20096 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003049762-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1319
ID   ABO47002 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003049765-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1320
ID   ABO47307 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1321
ID   ADA83571 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049752-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1322
ID   ABR71738 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003032133-A1.
PD   13-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;

     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1323
ID   ABR72348 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003032136-A1.
PD   13-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1324
ID   ABR98687 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036129-A1.
PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1325
ID   ABO07057 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003040053-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1326
ID   ABR85010 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040057-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1327
ID   ABR73568 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054467-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1328
ID   ABR76662 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003044932-A1.
PD   06-MAR-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1329
ID   ABR73263 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003022270-A1.
PD   06-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1330
ID   ABM18329 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054469-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1331
ID   ABO20788 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032126-A1.
PD   13-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity   30.7%;   Pred. No. 0.00033;

RESULT 1332
ID   ABO25531 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003054463-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1333
ID ABO25836 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1334
ID ABR94245 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1335
ID ABR80152 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1336
ID ABM11492 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1337
ID ABO33099 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1338
ID ABO30805 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1339
ID ABO31110 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1340
ID ABM27416 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1341
ID ABM30161 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1342

ID ABM05697 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1343
ID ABM15762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1344
ID ABM08747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1345
ID ABO42447 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1346
ID ABO38177 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1347
ID ABO46087 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1348
ID ABM66890 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1349
ID ADB20614 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1350
ID ABM19791 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00033;
RESULT 1351
ID ABO49503 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.

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PN   US2003049774-A1
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1352
ID   ABO49808 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049775-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1353
ID   ADA78866 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003073181-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1354
ID   ABR88365 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068720-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1355
ID   ABM27111 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068739-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1356
ID   ABM03508 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068763-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1357
ID   ABO40007 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068689-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1358
ID   ABO50113 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049776-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 6;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1359
ID   ABO51028 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049780-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1360
ID   ABO05484 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036126-A1.

PD   20-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1361
ID   ABR74788 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003044924-A1.
PD   06-MAR-2003.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1362
ID   ABR77267 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003044927-A1.
PD   06-MAR-2003.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1363
ID   ABM18024 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040072-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1364
ID   ABR96075 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040073-A1.
PD   27-FEB-2003.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1365
ID   ABO22008 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003054475-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1366
ID   ABO20178 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003032124-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1367
ID   ABO24481 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003064467-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1368
ID   ABR86230 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064455-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1369
ID   ABM10882 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064759-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%;   Score 134.5;   DB 7;   Length 198;
     Best Local Similarity 30.7%;   Pred. No. 0.00033;
RESULT 1370
ID   ABM76881 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN   US2003054465-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1371
ID   ABR89585 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073170-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1372
ID   ABM12712 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073176-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1373
ID   ABM06002 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068717-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1374
ID   ABO35127 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003068728-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1375
ID   ABM03203 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068764-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1376
ID   ABM19181 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104550-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1377
ID   ABM19486 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104551-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1378
ID   ABO46697 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003049761-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1379
ID   ABO49198 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049757-A1.
PD   13-MAR-2003.

PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1380
ID   ABR69241 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003027273-A1.
PD   06-FEB-2003.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1381
ID   ABR89280 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036119-A1.
PD   20-FEB-2003.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1382
ID   ABR72653 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036120-A1.
PD   20-FEB-2003.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1383
ID   ABR74483 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003036161-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1384
ID   ABO18751 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003044921-A1.
PD   06-MAR-2003.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1385
ID   ABR80457 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049739-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1386
ID   ABM01678 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003059882-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1387
ID   ABM02288 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003059884-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1388
ID   ABR87450 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068687-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 134.5; DB 7; Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1389
ID   ABM13017 standard; protein; 198 AA.

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DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073186-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1390
ID   ABM30771 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064443-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1391
ID   ABM24671 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003064444-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1392
ID   ABO29585 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068697-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1393
ID   ABO31415 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068710-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1394
ID   ABM14542 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068686-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1395
ID   ABM09967 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073178-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1396
ID   ABM39092 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068774-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1397
ID   ABM34857 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104538-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1398
ID   ABO51333 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049781-A1.


PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1399
ID   ABO04159 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003036158-A1.
PD   20-FEB-2003.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1400
ID   ABO10629 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003036151-A1.
PD   20-FEB-2003.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1401
ID   ABR77872 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003040067-A1.
PD   27-FEB-2003.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1402
ID   ABR79082 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054456-A1.
PD   20-MAR-2003.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1403
ID   ABO24176 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003054482-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1404
ID   ABR93940 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003054457-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1405
ID   ABM01983 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003059983-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1406
ID   ABM78406 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003049764-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1407
ID   ABR90195 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003073177-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match             7.6%;  Score 134.5; DB 7;  Length 198;
     Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1408
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ID ABM27721 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1409
ID ABM13322 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1410
ID ABO32025 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1411
ID ABM14237 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068683-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1412
ID ABM08442 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1413
ID ABO40312 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1414
ID ABM74747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1415
ID ABM33942 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1416
ID ABM20401 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1417
ID ABO48893 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049756-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1418
ID ABR72958 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036122-A1.
PD 20-FEB-2003.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1419
ID ABO15600 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1420
ID ABR85315 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040065-A1.
PD 27-FEB-2003.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1421
ID ABO15295 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044919-A1.
PD 06-MAR-2003.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1422
ID ABO17430 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040077-A1.
PD 27-FEB-2003.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1423
ID ABM17719 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044928-A1.
PD 06-MAR-2003.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1424
ID ABR85620 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1425
ID ABM77186 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1426
ID ABO28365 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   7.6%; Score 134.5; DB 7; Length 198;
    Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1427
ID ABM23146 standard; protein; 198 AA.

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DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068757-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1428
ID   ABM30466 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068723-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1429
ID   ABM21926 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068741-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1430
ID   ABM21621 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068744-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1431
ID   ABM15152 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068766-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1432
ID   ABO41227 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068694-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1433
ID   ABO36957 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068715-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1434
ID   ABO37567 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003068726-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1435
ID   ABM75357 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003104544-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1436
ID   ABM33637 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN   US2003096357-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1437
ID   AB046392 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003049760-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1438
ID   ADA82937 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003049755-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1439
ID   ABM31991 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068680-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1440
ID   ABM31381 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068762-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1441
ID   ADB86245 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003054472-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1442
ID   ABM32296 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068708-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1443
ID   ABM32601 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068713-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1444
ID   ABM31686 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068761-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1445
ID   ABM31076 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US2003068771-A1.
PD   10-APR-2003.

PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1446
ID   ADD05975 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003087376-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1447
ID   ADG02970 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003207397-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1448
ID   ADG01677 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003207399-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1449
ID   ADF95852 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003207398-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1450
ID   ADG12667 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003207392-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1451
ID   ADH09327 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003207395-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1452
ID   ADL33106 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003207396-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1453
ID   ADM30642 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003073813-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 7; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1454
ID   ADE74639 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003211572-A1.
PD   13-NOV-2003.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;

RESULT 1455
ID   ADF75251 standard; protein; 198 AA.
DE   Human secreted/transmembrane protein (PRO) #251.
PN   US2003211574-A1.
PD   13-NOV-2003.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1456
ID   ADF96464 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003215909-A1.
PD   20-NOV-2003.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1457
ID   ADG04735 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003215912-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1458
ID   ADG00895 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003215911-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1459
ID   ADG83151 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003215910-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1460
ID   ADH26432 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US2003068770-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1461
ID   ADH33401 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2003068768-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1462
ID   ADJ55140 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2004023321-A1.
PD   05-FEB-2004.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1463
ID   ADJ64911 standard; protein; 198 AA.
DE   Human PRO polypeptide #251.
PN   US2004038337-A1.
PD   26-FEB-2004.
PA   (GETH) GENENTECH INC.
      Query Match   7.6%; Score 134.5; DB 8; Length 198;
      Best Local Similarity   30.7%; Pred. No. 0.00033;
RESULT 1464
ID   ADM31807 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.

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PN   US200404834-A1
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 8;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1465
ID   ADM36854 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US200405358-A1.
PD   18-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 8;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1466
ID   ADM40659 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US200404835-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 8;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1467
ID   ADN38267 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US200409959-A1.
PD   13-MAY-2004.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 8;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1468
ID   AED50497 standard; protein; 198 AA.
DE   Novel human secreted and transmembrane protein PRO4421.
PN   US200516376-A1.
PD   28-JUL-2005.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 9;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1469
ID   AEG63189 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US200607354-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 10;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1470
ID   AEG73012 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US200607426-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 10;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1471
ID   AEG62577 standard; protein; 198 AA.
DE   Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN   US200607354-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 10;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1472
ID   AEG88494 standard; protein; 198 AA.
DE   Human PRO protein amino acid sequence - SEQ ID 502.
PN   US200607422-A1.
PD   06-APR-2006.
PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 10;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1473
ID   AEH17810 standard; protein; 198 AA.
DE   Human tumor overexpressed cDNA protein product PRO4421 SEQ ID NO: 502.
PN   US200609864-A1.
PD   04-MAY-2006.

PA   (GETH ) GENENTECH INC.
     Query Match        7.6%;   Score 134.5;  DB 10;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1474
ID   AEK56718 standard; protein; 198 AA.
DE   Human PRO polypeptide SEQ ID NO:136.
PN   WO200609887-A2.
PD   21-SEP-2006.
PA   (GETH ) GENENTECH INC.
PA   (LEXI-) LEXICON GENETICS INC.
     Query Match        7.6%;   Score 134.5;  DB 10;  Length 198;
     Best Local Similarity  30.7%;   Pred. No. 0.00033;
RESULT 1475
ID   ADE63380 standard; protein; 240 AA.
DE   Rat Protein P10252, SEQ ID NO 9319.
PN   WO200301647-A2.
PD   27-FEB-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
     Query Match        7.6%;   Score 134;  DB 7;  Length 240;
     Best Local Similarity  24.6%;   Pred. No. 0.00049;
RESULT 1476
ID   AEC12927 standard; protein; 240 AA.
DE   Rat biomarker of neurotrophic agent protein SEQ ID NO 1273.
PN   WO200508312-A2.
PD   09-SEP-2005.
PA   (BIOJ ) BIOGEN IDEC MA INC.
     Query Match        7.6%;   Score 134;  DB 9;  Length 240;
     Best Local Similarity  24.6%;   Pred. No. 0.00049;
RESULT 1477
ID   ADV90298 standard; protein; 327 AA.
DE   Protease-hydrolysed polypeptide #75.
PN   WO200411352-A1.
PD   29-DEC-2004.
PA   (DIRE-) DIREVO BIOTECH AG.
     Query Match        7.5%;   Score 133.5;  DB 9;  Length 327;
     Best Local Similarity  22.7%;   Pred. No. 0.00086;
RESULT 1478
ID   AEJ42183 standard; protein; 327 AA.
DE   Human T-cell surface antigen CD2 precursor.
PN   WO200607198-A2.
PD   29-JUN-2006.
PA   (DIRE-) DIREVO BIOTECH AG.
PA   (VOET/) VOETSMEIER C.
     Query Match        7.5%;   Score 133.5;  DB 10;  Length 327;
     Best Local Similarity  22.7%;   Pred. No. 0.00086;
RESULT 1479
ID   AAR74221 standard; protein; 332 AA.
DE   Epitope on the primary CD2 sequence.
PN   US5411861-A.
PD   02-MAY-1995.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match        7.5%;   Score 133.5;  DB 2;  Length 332;
     Best Local Similarity  22.7%;   Pred. No. 0.00088;
RESULT 1480
ID   AAY30457 standard; protein; 332 AA.
DE   Predicted sequence of the mature CD2 protein.
PN   US5955264-A.
PD   21-SEP-1999.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match        7.5%;   Score 133.5;  DB 2;  Length 332;
     Best Local Similarity  22.7%;   Pred. No. 0.00088;
RESULT 1481
ID   ADA25185 standard; protein; 332 AA.
DE   Mature CD2 protein.
PN   US6579676-B1.
PD   17-JUN-2003.
PA   (GEHO ) GEN HOSPITAL CORP.
     Query Match        7.5%;   Score 133.5;  DB 6;  Length 332;
     Best Local Similarity  22.7%;   Pred. No. 0.00088;
RESULT 1482
ID   AARl1921 standard; protein; 351 AA.
DE   Human Tll sugar protein.
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PN JP03035782-A.
PD 15-FEB-1991.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 24.4%; Pred. No. 0.00096;
RESULT 1483
ID AAR20803 standard; protein; 351 AA.
DE Human CD2 antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1484
ID AAR34223 standard; protein; 351 AA.
DE Amino acid sequence of CD2.
PN WO9306852-A2.
PD 15-APR-1993.
PA (BIOJ) BIOGEN INC.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 23.6%; Pred. No. 0.00096;
RESULT 1485
ID AAR91431 standard; protein; 351 AA.
DE Human CD2.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1486
ID AAW80440 standard; protein; 351 AA.
DE Human CD2 antigen.
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1487
ID AAW86188 standard; protein; 351 AA.
DE Human CD2 antigen.
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1488
ID AAY96126 standard; protein; 351 AA.
DE Human cell surface antigen CD2.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 3; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1489
ID AAU02435 standard; protein; 351 AA.
DE Human lymphocyte cell surface antigen CD2 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 4; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1490
ID ADD25530 standard; protein; 351 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #42.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENECRAFT INC.
Query Match 7.5%; Score 133.5; DB 7; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1491
ID ADF76723 standard; protein; 351 AA.
DE Novel human secreted and transmembrane protein SeqID 398.
PN WO2003072035-A2.

PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 7; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1492
ID ADO49339 standard; protein; 351 AA.
DE Human CD2 antigen.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 7.5%; Score 133.5; DB 8; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1493
ID ADQ18464 standard; protein; 351 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1283.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.5%; Score 133.5; DB 8; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1494
ID ADP56034 standard; protein; 351 AA.
DE Human PRO protein sequence SEQ ID NO:2010.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 8; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1495
ID ADY19602 standard; protein; 351 AA.
DE PRO polypeptide SEQ ID NO 5408.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 9; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1496
ID ADY15634 standard; protein; 351 AA.
DE PRO polypeptide SEQ ID NO 1440.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH) GENENTECH INC.
Query Match 7.5%; Score 133.5; DB 9; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00096;
RESULT 1497
ID AAP81178 standard; protein; 360 AA.
DE Sequence of human T11 sheep erythrocyte glycoprotein (T11) cDNA deduced
DE from PB1.
PN EP260880-A.
PD 23-MAR-1988.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 7.5%; Score 133.5; DB 1; Length 360;
Best Local Similarity 23.9%; Pred. No. 0.00099;
RESULT 1498
ID AAB43688 standard; protein; 737 AA.
DE Human cancer associated protein sequence SEQ ID NO:1133.
PN WO2005055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.5%; Score 133.5; DB 3; Length 737;
Best Local Similarity 22.3%; Pred. No. 0.0028;
RESULT 1499
ID ABU04810 standard; protein; 737 AA.
DE Human expressed protein tag (EPT) #1476.

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PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
     Query Match        7.5%;   Score 133.5;  DB 6;   Length 737;
     Best Local Similarity  22.3%;   Pred. No. 0.0028;
RESULT 1500
ID   AAR28366 standard; protein; 225 AA.
DE   Sheep LFA-3 protein.
PN   EP517174-A2.
PD   09-DEC-1992.
PA   (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.
     Query Match        7.4%;   Score 131;  DB 2;   Length 225;
     Best Local Similarity  25.0%;   Pred. No. 0.00087;
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                 GenCore version 6.2
      Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:    March 29, 2007, 02:25:23 ; Search time 53 Seconds
                                     (without alignments)
                                     553.260 Million cell updates/sec

Title:           US-10-063-549-46
Perfect score:   1772
Sequence:        1 MAGSPTCLTLIYILWQLTGS..........PHSLLTMPDTPRLFAYENVI 335

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        650591 seqs, 8753062B residues

Total number of hits satisfying chosen parameters:      650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries
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Database :   Issued Patents AA:*
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        3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
        4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
        5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
        6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
        7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1772	100.0	335	2	US-09-991-181-253	Sequence 253, App
2	1772	100.0	335	2	US-09-990-444-253	Sequence 253, App
3	1772	100.0	335	2	US-09-997-333-253	Sequence 253, App
4	1772	100.0	335	2	US-09-992-598-253	Sequence 253, App
5	1772	100.0	335	3	US-09-989-735-253	Sequence 253, App
6	1772	100.0	335	3	US-09-989-726-253	Sequence 253, App
7	1772	100.0	335	3	US-09-997-514-253	Sequence 253, App
8	1772	100.0	335	3	US-09-989-728-253	Sequence 253, App
9	1772	100.0	335	3	US-09-997-349-253	Sequence 253, App
10	1772	100.0	335	3	US-09-997-653-253	Sequence 253, App
11	1772	100.0	335	3	US-09-989-293A-253	Sequence 253, App
12	498	28.1	97	2	US-09-513-99C-4472	Sequence 4472, Ap
13	362.5	20.5	328	2	US-09-949-016-6428	Sequence 6428, App
14	362.5	20.5	329	2	US-09-149-476-483	Sequence 483, App
15	362.5	20.5	332	2	US-09-949-016-7327	Sequence 7327, Ap
16	316.5	17.9	331	3	US-10-127-413-2	Sequence 2, Appli
17	186	10.5	343	1	US-08-348-792-10	Sequence 10, Appli
18	186	10.5	343	1	US-08-462-738-10	Sequence 10, Appli
19	186	10.5	343	2	US-09-199-955-10	Sequence 10, Appli
20	186	10.5	343	2	US-08-880-875-10	Sequence 10, Appli
21	182.5	10.3	335	2	US-08-348-792-2	Sequence 2, Appli
22	182.5	10.3	335	1	US-08-462-738-2	Sequence 2, Appli
23	182.5	10.3	335	2	US-09-199-955-2	Sequence 2, Appli
24	182.5	10.3	335	2	US-08-880-875-2	Sequence 2, Appli
25	182.5	10.3	335	2	US-09-369-248A-3	Sequence 3, Appli
26	182.5	10.3	335	2	US-09-949-002-349	Sequence 349, App
27	182.5	10.3	335	3	US-10-062-523-3	Sequence 3, Appli
28	182.5	10.3	351	2	US-09-949-002-418	Sequence 418, App
29	180	10.2	307	1	US-08-348-792-8	Sequence 8, Appli
30	180	10.2	307	1	US-08-462-738-8	Sequence 8, Appli
31	180	10.2	307	2	US-09-199-955-8	Sequence 8, Appli
32	180	10.2	307	2	US-08-880-875-8	Sequence 8, Appli
33	170	9.6	365	2	US-09-949-016-6907	Sequence 6907, Ap
34	170	9.6	391	2	US-09-949-016-7325	Sequence 7325, Ap
35	164.5	9.3	305	1	US-08-348-792-6	Sequence 6, Appli
36	164.5	9.3	305	1	US-08-462-738-6	Sequence 6, Appli
37	164.5	9.3	305	2	US-09-199-955-6	Sequence 6, Appli
38	164.5	9.3	305	2	US-08-880-875-6	Sequence 6, Appli
39	158.5	8.9	329	1	US-08-348-792-12	Sequence 12, Appl
40	158.5	8.9	329	1	US-08-462-738-12	Sequence 12, Appl
41	158.5	8.9	329	2	US-09-199-955-12	Sequence 12, Appl
42	158.5	8.9	329	2	US-08-880-875-12	Sequence 12, Appl
43	152	8.6	298	1	US-08-348-792-4	Sequence 4, Appli
44	152	8.6	298	2	US-08-462-738-4	Sequence 4, Appli
45	152	8.6	298	2	US-09-199-955-4	Sequence 4, Appli
46	152	8.6	298	2	US-08-880-875-4	Sequence 4, Appli
47	150.5	8.5	285	3	US-09-369-248A-2	Sequence 2, Appli
48	150.5	8.5	285	2	US-10-062-523-2	Sequence 2, Appli
49	141	8.0	149	3	US-09-227-357-443	Sequence 443, App
50	141	8.0	149	1	US-09-973-278-571	Sequence 571, App
51	140.5	7.9	142	2	US-09-973-278-252	Sequence 252, App
52	140.5	7.9	143	2	US-09-227-357-192	Sequence 192, App
53	136.5	7.7	351	2	US-08-466-465-6	Sequence 6, Appli
54	136.5	7.7	351	2	US-09-730-465-6	Sequence 6, Appli
55	128	7.2	225	3	US-08-328-152A-31	Sequence 31, Appl
56	128	7.2	321	7	5169835-17	Patent No. 5169835
57	126	7.1	427	2	US-10-062-523-16	Sequence 16, Appl
58	125.5	7.1	464	2	US-08-602-725-32	Sequence 32, Appl
59	125.5	7.1	464	2	US-09-949-016-6116	Sequence 6116, Ap
60	125.5	7.1	464	2	US-09-949-016-7525	Sequence 7525, Ap
61	124.5	7.0	365	2	US-09-949-016-7591	Sequence 7591, Ap
62	123	6.9	199	3	US-08-328-152A-36	Sequence 36, Appl
63	123	6.9	223	3	US-10-062-523-19	Sequence 19, Appl
64	122	6.9	316	2	US-09-397-243D-13	Sequence 13, Appl
65	120	6.8	352	3	US-09-991-181-505	Sequence 505, App
66	120	6.8	352	2	US-09-990-444-505	Sequence 505, App
67	120	6.8	352	2	US-09-997-333-505	Sequence 505, App
68	120	6.8	352	2	US-09-992-598-505	Sequence 505, App
69	120	6.8	352	2	US-09-989-735-505	Sequence 505, App
70	120	6.8	352	2	US-09-989-726-505	Sequence 505, App
71	120	6.8	352	3	US-09-997-514-505	Sequence 505, App
72	120	6.8	352	3	US-09-989-728-505	Sequence 505, App
73	120	6.8	352	3	US-09-997-349-505	Sequence 505, App
74	120	6.8	352	3	US-09-997-653-505	Sequence 505, App
75	120	6.8	352	3	US-09-989-293A-505	Sequence 505, App
76	119.5	6.7	365	1	US-08-979-424-3	Sequence 3, Appli
77	119.5	6.7	365	2	US-09-272-496-2	Sequence 2, Appli
78	119.5	6.7	365	2	US-09-949-016-6064	Sequence 6064, Ap
79	119.5	6.7	383	2	US-09-949-016-11050	Sequence 11050, A
80	119.5	6.7	418	2	US-08-630-172-18	Sequence 18, Appl
81	119.5	6.7	418	2	US-09-375-419-18	Sequence 18, Appl
82	117.5	6.6	344	1	US-08-602-725-34	Sequence 34, Appl
83	117.5	6.6	365	3	US-08-928-383B-2	Sequence 2, Appl
84	116.5	6.6	319	1	US-08-597-495B-22	Sequence 22, Appl
85	116.5	6.6	319	2	US-08-068-051A-22	Sequence 22, Appl
86	116.5	6.6	319	2	US-09-336-536-67	Sequence 67, Appl
87	116.5	6.6	319	2	US-09-254-465A-6	Sequence 6, Appli
88	116.5	6.6	319	1	US-09-953-499-6	Sequence 6, Appli
89	115.5	6.5	184	2	US-09-375-419-2	Sequence 2, Appli
90	115.5	6.5	184	1	US-08-217-299-1	Sequence 1, Appli
91	114.5	6.5	642	1	US-08-602-725-36	Sequence 36, Appl
92	114.5	6.5	698	2	US-09-949-016-6484	Sequence 6484, Ap
93	114.5	6.5	702	1	US-08-389-459A-17	Sequence 17, Appl
94	114.5	6.5	734	1	US-08-987-867A-17	Sequence 17, Appl
95	114.5	6.5	740	1	US-09-949-016-8168	Sequence 8168, Ap
96	114.5	6.5	740	2	US-09-991-181-503	Sequence 503, App
97	113	6.4	373	2	US-09-181-503	Sequence 503, App
98	113	6.4	373	3	US-09-999-833A-59	Sequence 59, Appl
99	113	6.4	373	2	US-09-990-444-503	Sequence 503, App

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103	113	6.4	373	2	US-09-989-735-503	Sequence 503, Appl
104	113	6.4	373	2	US-09-978-189-59	Sequence 59, Appl
105	113	6.4	373	2	US-10-017-085A-59	Sequence 59, Appl
106	113	6.4	373	2	US-09-989-726-503	Sequence 503, App
107	113	6.4	373	3	US-10-145-129A-59	Sequence 59, App
108	113	6.4	373	3	US-09-997-514-503	Sequence 503, Appl
109	113	6.4	373	3	US-10-013-929A-59	Sequence 59, Appl
110	113	6.4	373	3	US-09-989-728-503	Sequence 503, App
111	113	6.4	373	3	US-10-013-917A-59	Sequence 59, Appl
112	113	6.4	373	3	US-09-997-349-503	Sequence 503, Appl
113	113	6.4	373	3	US-09-997-653-503	Sequence 503, App
114	113	6.4	373	3	US-09-989-293A-503	Sequence 503, App
115	111.5	6.3	174	1	US-08-765-536-2	Sequence 2, Appli
116	111.5	6.3	174	5	PCT-US95-08401-2	Sequence 2, Appli
117	110.5	6.2	365	2	US-09-899-634C-4	Sequence 4, Appli
118	109.5	6.2	315	2	US-09-910-174B-28	Sequence 28, Appl
119	109.5	6.2	315	2	US-09-620-461-28	Sequence 28, Appl
120	109	6.2	324	2	US-09-910-174B-6	Sequence 6, Appli
121	109	6.2	324	2	US-09-620-461-6	Sequence 6, Appli
122	105.5	6.0	323	2	US-09-651-200-21	Sequence 21, Appl
123	105.5	6.0	323	2	US-09-441-411-22	Sequence 22, Appl
124	105.5	6.0	323	2	US-09-915-789A-16	Sequence 16, Appl
125	105.5	6.0	323	5	PCT-US94-09642-2	Sequence 2, Appli
126	105.5	6.0	329	2	US-08-456-104-2	Sequence 2, Appli
127	105.5	6.0	329	2	US-08-101-624-2	Sequence 2, Appli
128	105.5	6.0	329	2	US-08-479-744A-2	Sequence 2, Appli
129	105.5	6.0	329	2	US-08-280-757B-2	Sequence 2, Appli
130	105.5	6.0	329	2	US-08-205-697A-23	Sequence 23, Appl
131	105.5	6.0	329	2	US-08-702-525-23	Sequence 23, Appl
132	105.5	6.0	329	2	US-08-403-253A-4	Sequence 4, Appli
133	105.5	6.0	329	2	US-08-435-816A-4	Sequence 4, Appli
134	105.5	6.0	329	2	US-09-425-762-2	Sequence 2, Appli
135	105.5	6.0	372	2	US-09-837-867A-23	Sequence 23, Appl
136	105.5	6.0	329	2	US-09-906-132-2	Sequence 2, Appli
137	105.5	5.9	329	2	US-09-206-132-2	Sequence 2, Appli
138	105.5	5.9	329	2	US-09-441-411-26	Sequence 26, Appl
139	104.5	5.9	144	2	US-09-425-516-2	Sequence 2, Appli
140	104	5.8	349	2	US-09-350-202-4	Sequence 4, Appli
141	102	5.7	503	2	US-08-592-711-4	Sequence 4, Appli
142	101.5	5.7	773	2	US-08-349-915B-4	Sequence 4, Appli
143	101.5	5.7	773	5	PCT-US95-02576-23	Sequence 23, Appl
144	101.5	5.7	372	2	US-09-949-016-11132	Sequence 11132, A
145	101.5	5.6	329	2	US-09-906-132-2	Sequence 2, Appli
146	104.5	5.6	349	2	US-09-667-135-32	Sequence 32, Appl
147	104	5.5	503	2	US-09-924-103-4	Sequence 4, Appli
148	102	5.5	144	5	US-09-513-999C-4353	Sequence 4353, Ap
149	101.5	5.5	270	2	US-09-254-465A-24	Sequence 24, Appl
150	101.5	5.5	273	2	US-09-953-499-24	Sequence 24, Appl
151	101.5	5.5	273	2	US-09-254-465A-26	Sequence 26, Appl
152	100.5	5.4	273	2	US-09-953-499-26	Sequence 26, Appl
153	100.5	5.4	638	2	US-09-228-986-74	Sequence 74, Appl
154	100	5.4	638	2	US-10-101-464A-74	Sequence 74, Appl
155	98.5	5.4	365	3	US-08-928-383B-24	Sequence 24, Appl
156	98.5	5.4	732	3	US-08-928-383B-23	Sequence 23, Appl
157	98	5.4	503	2	US-09-818-247-5	Sequence 5, Appli
158	97	5.4	773	2	US-08-999-689A-6	Sequence 6, Appli
159	97	5.4	773	2	US-09-944-807-4	Sequence 4, Appli
160	97	5.4	503	2	US-09-312-157-2	Sequence 2, Appli
161	97	5.4	773	2	US-09-717-888-2	Sequence 2, Appli
162	97	5.4	773	2	US-09-818-247-2	Sequence 2, Appli
163	96.5	5.4	534	2	US-09-953-499-24	Sequence 24, Appl
164	96.5	5.4	534	2	US-09-651-200-6	Sequence 6, Appli
165	96.5	5.4	534	2	US-09-875-338-7	Sequence 7, Appli
166	96.5	5.4	698	2	US-09-875-338-9	Sequence 9, Appli
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168	96	5.4	441	2	US-09-651-200-4	Sequence 4, Appli
169	96	5.4	526	2	US-09-910-174B-9	Sequence 9, Appli
170	96	5.4	526	2	US-09-620-461-9	Sequence 9, Appli
171	96	5.4	526	2	US-09-949-016-6122	Sequence 6122, Ap
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189	93	5.2	316	2	US-09-620-461-24	Sequence 24, Appl
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193	92.5	5.2	299	2	US-09-188-930-331	Sequence 331, App
194	92.5	5.2	299	2	US-09-462-270-2	Sequence 2, Appli
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198	92.5	5.2	299	2	US-09-907-794A-119	Sequence 119, App
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254	5.1	90	541	2	US-09-949-002-360	Sequence 360, App
255	5.1	90	541	3	US-10-157-447-2	Sequence 2, Appli
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257	5.1	90	821	2	US-08-836-734E-8	Sequence 8, Appli
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395	85	4.8	821	2	US-09-622-880B-15	Sequence 8, Appli
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435	83.5	4.7	408	2	US-09-724-864-62	Sequence 62, Appl
436	83.5	4.7	450	2	US-09-907-794A-320	Sequence 320, App
437	83.5	4.7	450	2	US-09-905-125A-320	Sequence 320, App
438	83.5	4.7	450	2	US-09-902-775A-320	Sequence 320, App
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448	83.5	4.7	450	2	US-09-904-462-320	Sequence 320, App
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457	83.5	4.7	789	2	US-09-589-477-96	Sequence 96, Appl
458	83.5	4.7	789	2	US-10-099-285A-96	Sequence 96, Appl
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460	83	4.7	1501	1	US-08-716-679-3	Sequence 3, Appli
461	83	4.7	342	2	US-09-401-636-5	Sequence 5, Appli
462	83	4.7	464	2	US-09-297-468-2	Sequence 2, Appli
463	83	4.7	514	3	US-10-094-749-3035	Sequence 3035, Ap
464	83	4.7	757	2	US-09-818-247-2	Sequence 2, Appli

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514	81.5	4.6	352	2	US-10-020-445A-612	Sequence 612, App
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536	81.5	4.6	1441	2	US-09-949-016-10397	Sequence 10397, A
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541	4.6	81	304	US-08-414-657D-44	Sequence 44, Appl
542	4.6	81	308	US-08-414-657D-46	Sequence 46, Appl
543	4.6	81	325	US-08-414-657D-2	Sequence 2, Appli
544	4.6	81	325	US-08-414-657D-41	Sequence 41, Appl
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547	4.6	81	338	US-08-414-657D-8	Sequence 8, Appli
548	4.6	81	829	US-09-135-080-8	Sequence 8, Appl
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550	4.6	81	205	US-09-975-723A-1	Sequence 1, Appl
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552	4.5	80.5	313	US-09-915-789A-18	Sequence 18, Appl
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556	4.5	80.5	346	US-08-460-741-2	Sequence 2, Appli
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577	4.5	80	315	US-08-414-657D-47	Sequence 47, Appl
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579	4.5	80	338	US-08-414-657D-43	Sequence 43, Appl
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615	544	4.4	78.5	US-10-020-445A-259	Sequence 259, App
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622	847	4.4	78.5	US-09-002-328	Sequence 328, App
623	857	4.4	78.5	US-09-248-796A-20522	Sequence 20522, A
624	341	4.4	78	US-09-002-427	Sequence 427, App
625	345	4.4	78	US-08-248-628A-2	Sequence 2, Appl
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627	624	4.4	78	US-09-949-016-10547	Sequence 10547, A
628	624	4.4	78	US-08-642-406A-22	Sequence 22, Appl
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652	650	4.4	77.5	US-09-949-002-390	Sequence 390, App
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654	662	4.4	77.5	US-08-261-304-7	Sequence 7, Appl
655	677	4.4	77.5	US-09-949-002-416	Sequence 416, App
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678	4866	4.3	77	US-09-252-991A-20611	Sequence 2611, A
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681	490	4.3	76.5	US-08-896-537A-3	Sequence 3, Appli
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683		4.3	76.5	US-09-866-510-12	Sequence 12, Appl

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703	4.3	76.5	1089	2	US-09-866-510-6	Sequence 6, Appli
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705	4.3	76.5	1089	2	US-09-784-358-16	Sequence 16, Appl
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707	4.3	76.5	1089	2	US-09-949-016-6703	Sequence 6703, Ap
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716	4.3	76.5	1723	2	US-09-194-612A-31	Sequence 31, Appl
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851	73	4.1	548	2	US-09-900-797-12	Sequence 12, Appl
852	73	4.1	548	2	US-09-893-820-12	Sequence 12, Appl
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855	73	4.1	651	2	US-08-985-950-22	Sequence 22, Appl
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967	72	4.1	1745	2	US-09-065-474-33	Sequence 33, Appl
968	72	4.1	1745	2	US-09-557-034-33	Sequence 33, Appl
969	72	4.1	2383	2	US-09-492-709A-302	Sequence 302, App
970	72	4.1	2753	2	US-09-949-016-7659	Sequence 7659, Ap
971	72	4.1	2753	2	US-09-949-016-7660	Sequence 7660, Ap
972	72	4.1	2780	2	US-10-220-587-2	Sequence 2, Appli
973	72	4.1	4872	2	US-09-424-783-3	Sequence 3, Appli
974	71.5	4.0	206	2	US-08-821-994-77	Sequence 77, Appl
975	71.5	4.0	241	2	US-09-248-796A-17942	Sequence 17942, A

976	7	4.0	71.5	248	519835-15	Patent No. 5169835
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978	2	4.0	71.5	327	US-09-173-581-5	Sequence 5, Appli
979	2	4.0	71.5	327	US-09-420-915-5	Sequence 5, Appli
980	2	4.0	71.5	333	US-09-949-002-502	Sequence 502, App
981	2	4.0	71.5	384	US-09-552-322-2	Sequence 2, Appli
982	2	4.0	71.5	403	US-09-638-649-5	Sequence 5, Appli
983	2	4.0	71.5	403	US-09-638-648-5	Sequence 5, Appli
984	2	4.0	71.5	456	US-09-248-796A-23791	Sequence 23791, A
985	2	4.0	71.5	462	US-09-166-350-18	Sequence 18, Appl
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992	2	4.0	71.5	746	US-09-717-888-4	Sequence 4, Appli
993	2	4.0	71.5	764	US-09-949-016-6254	Sequence 6254, Ap
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995	2	4.0	71.5	816	US-09-949-016-8119	Sequence 8119, Ap
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997	2	4.0	71.5	933	US-09-979-195-2	Sequence 2, Appli
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1048	2	4.0	71	240	US-09-136-389-148	Sequence 148, App

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1051	2	71	4.0	240	US-09-711-485-147	Sequence 147, App
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1067	1	71	4.0	687	US-08-786-164-6	Sequence 6, Appli
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1074	2	71	4.0	758	US-10-105-901A-1	Sequence 1, Appli
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1077	2	71	4.0	780	US-08-786-164-14	Sequence 14, Appl
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1081	2	71	4.0	906	US-09-650-855-13	Sequence 13, Appl
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1103	2	71	4.0	1481	US-08-944-868A-40	Sequence 40, Appl
1104	2	71	4.0	1481	US-08-944-423A-40	Sequence 40, Appl
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1109	2	70.5	4.0	223	US-09-303-518D-776	Sequence 776, App
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1114	2	70.5	4.0	334	US-09-438-185A-452	Sequence 452, App
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1132	2	70.5	4.0	617	US-09-188-930-303	Sequence 303, App
1133	2	70.5	4.0	617	US-09-312-283C-303	Sequence 303, App
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1143	2	70.5	4.0	767	US-09-348-886-2	Sequence 2, Appli
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1146	1	70.5	4.0	788	US-08-786-164-15	Sequence 15, Appl
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1149	2	70.5	4.0	940	US-09-438-185A-468	Sequence 468, App
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1156	2	70.5	4.0	1088	US-08-484-719B-6	Sequence 6, Appli
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1167	2	70	4.0	126	US-09-848-798-146	Sequence 146, App
1168	2	70	4.0	167	US-08-821-994-43	Sequence 43, Appl
1169	2	70	4.0	282	US-09-602-787A-162	Sequence 162, App
1170	2	70	4.0	282	US-09-602-787A-164	Sequence 164, App
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1174	2	70	4.0	320	US-09-603-207-14	Sequence 14, Appl
1175	3	70	4.0	320	US-10-329-148A-14	Sequence 14, Appl
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1179	1	70	4.0	347	US-08-459-512-43	Sequence 43, Appl
1180	2	70	4.0	347	US-08-459-657-43	Sequence 43, Appl
1181	2	70	4.0	347	US-08-460-132-43	Sequence 43, Appl
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1183	2	70	4.0	347	US-08-730-465-8	Sequence 8, Appli
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1188	2	70	4.0	469	US-09-398-496-8	Sequence 8, Appli
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1193	2	70	4.0	548	US-09-398-395A-8	Sequence 8, Appli
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1222	70	4.0	576	2	US-08-924-376-4	Sequence 4, Appli
1223	70	4.0	576	2	US-08-685-212-4	Sequence 4, Appli
1224	70	4.0	576	2	US-09-173-151A-30	Sequence 30, Appl
1225	70	4.0	576	2	US-08-466-932A-4	Sequence 4, Appli
1226	70	4.0	576	5	PCT-US94-02414-4	Sequence 4, Appli
1227	70	4.0	582	2	PCT-US96-08899-4	Sequence 4, Appli
1228	70	4.0	590	2	US-09-147-405B-13	Sequence 13, Appl
1229	70	4.0	593	2	US-10-104-047-3415	Sequence 3415, Ap
1230	70	4.0	611	2	US-09-147-405B-11	Sequence 11, Appl
1231	70	4.0	611	2	US-07-757-342D-8	Sequence 8, Appli
1232	70	4.0	625	2	US-09-461-657B-8	Sequence 8, Appli
1233	70	4.0	629	2	US-09-134-001C-4504	Sequence 4504, Ap
1234	70	4.0	636	2	US-10-101-464A-927	Sequence 927, App
1235	70	4.0	636	2	US-07-757-342D-7	Sequence 7, Appli
1236	70	4.0	637	2	US-09-461-657B-7	Sequence 7, Appli
1237	70	4.0	652	2	US-09-569-611C-35	Sequence 35, Appl
1238	70	4.0	652	2	US-09-310-463-4	Sequence 4, Appli
1239	70	4.0	652	2	US-08-842-248A-4	Sequence 4, Appli
1240	70	4.0	687	5	US-10-143-618-4	Sequence 4, Appli
1241	70	4.0	750	2	PCT-US91-09784-2	Sequence 2, Appli
1242	70	4.0	783	2	US-10-094-749-2095	Sequence 2095, Ap
1243	70	4.0	837	1	US-08-780-562-7	Sequence 7, Appli
1244	70	4.0	894	2	US-07-923-976-2	Sequence 2, Appli
1245	70	4.0	894	1	US-08-599-455B-2	Sequence 2, Appli
1246	70	4.0	894	2	US-09-069-781B-2	Sequence 2, Appli
1247	70	4.0	894	2	US-08-618-957A-12	Sequence 12, Appl
1248	70	4.0	894	2	US-09-137-132-2	Sequence 2, Appli
1249	70	4.0	894	2	US-08-864-564A-2	Sequence 2, Appli
1250	70	4.0	894	2	US-09-094-410-2	Sequence 2, Appli
1251	70	4.0	894	2	US-08-708-123D-2	Sequence 2, Appli
1252	70	4.0	894	2	US-08-583-153A-2	Sequence 2, Appli
1253	70	4.0	894	2	US-08-570-142D-2	Sequence 2, Appli
1254	70	4.0	894	2	US-08-638-524B-2	Sequence 2, Appli
1255	70	4.0	894	2	US-10-095-929-12	Sequence 12, Appl
1256	70	4.0	894	2	US-09-950-149-2	Sequence 2, Appli
1257	70	4.0	944	2	US-09-449-285A-2	Sequence 2, Appli
1258	70	4.0	944	2	US-09-964-238-2	Sequence 2, Appli
1259	70	4.0	950	2	US-09-449-285A-4	Sequence 4, Appli
1260	70	4.0	950	2	US-09-964-238-4	Sequence 4, Appli
1261	70	4.0	1092	2	US-09-147-405B-15	Sequence 15, Appl
1262	70	4.0	1162	1	US-08-599-455B-43	Sequence 43, Appl
1263	70	4.0	1162	2	US-09-069-781B-43	Sequence 43, Appl
1264	70	4.0	1162	2	US-09-117-132-43	Sequence 43, Appl
1265	70	4.0	1162	2	US-08-864-564A-43	Sequence 43, Appl
1266	70	4.0	1162	2	US-09-094-410-43	Sequence 43, Appl
1267	70	4.0	1162	2	US-08-708-123D-43	Sequence 43, Appl

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1268	1162	2	US-08-638-524B-43	4.0	70	Sequence 43, Appl
1269	1162	2	US-09-950-149-43	4.0	70	Sequence 43, Appl
1270	1214	2	US-09-949-016-6885	4.0	70	Sequence 6885, Ap
1271	1318	2	US-09-949-016-7130	4.0	70	Sequence 7130, Ap
1272	1461	2	US-09-976-594-531	4.0	70	Sequence 531, Appl
1273	2183	2	US-08-746-111-5	4.0	70	Sequence 5, Appli
1274	223	2	US-09-303-518D-780	3.9	69.5	Sequence 780, App
1275	307	2	US-09-540-236-2790	3.9	69.5	Sequence 2790, Ap
1276	314	1	US-08-353-476-71	3.9	69.5	Sequence 71, Appl
1277	324	2	US-09-328-352-4577	3.9	69.5	Sequence 4577, Ap
1278	328	1	US-08-225-477B-5	3.9	69.5	Sequence 5, Appli
1279	328	5	PCT-US95-04353-5	3.9	69.5	Sequence 5, Appli
1280	333	1	US-08-436-463-6	3.9	69.5	Sequence 6, Appli
1281	333	1	US-08-024-253-6	3.9	69.5	Sequence 6, Appli
1282	334	1	US-09-134-000C-5207	3.9	69.5	Sequence 5207, Ap
1283	334	2	US-08-646-981-16	3.9	69.5	Sequence 16, Appl
1284	447	2	US-09-198-452A-972	3.9	69.5	Sequence 972, App
1285	456	2	US-09-438-185A-901	3.9	69.5	Sequence 901, App
1286	484	2	US-09-248-796A-15483	3.9	69.5	Sequence 15483, A
1287	496	2	US-10-104-047-3006	3.9	69.5	Sequence 3006, Ap
1288	499	2	US-09-049-672A-1	3.9	69.5	Sequence 1, Appli
1289	503	2	US-09-487-558B-424	3.9	69.5	Sequence 424, App
1290	506	2	US-08-888-998-2	3.9	69.5	Sequence 2, Appli
1291	506	2	US-09-362-633-2	3.9	69.5	Sequence 2, Appli
1292	506	2	US-09-377-476-2	3.9	69.5	Sequence 2, Appli
1293	506	2	US-09-877-476-28	3.9	69.5	Sequence 28, Appl
1294	512	2	US-09-877-476-36	3.9	69.5	Sequence 36, Appl
1295	548	2	US-09-248-796A-14219	3.9	69.5	Sequence 14219, A
1296	555	2	US-09-538-092-1058	3.9	69.5	Sequence 1058, Ap
1297	559	2	US-09-328-352-5873	3.9	69.5	Sequence 5873, Ap
1298	677	2	US-09-949-016-9137	3.9	69.5	Sequence 9137, Ap
1299	697	2	US-09-270-767-58094	3.9	69.5	Sequence 58094, A
1300	742	2	US-09-486-072-3	3.9	69	Sequence 3, Appli
1301	804	2	US-09-194-297A-4	3.9	69	Sequence 4, Appli
1302	847	2	US-08-981-446B-3	3.9	69	Sequence 3, Appli
1303	898	2	US-09-270-767-42783	3.9	69	Sequence 42783, A
1304	948	2	US-09-949-016-10987	3.9	69	Sequence 10987, A
1305	1033	1	US-10-363-937-13	3.9	69	Sequence 13, Appl
1306	1172	2	US-10-029-347-4	3.9	69	Sequence 4, Appli
1307	1260	2	US-09-712-363-176	3.9	69	Sequence 176, App
1308	1722	2	US-08-506-296B-21	3.9	69	Sequence 21, Appl
1309	1722	2	US-08-194-612A-1	3.9	69	Sequence 1, Appli
1310	1740	2	US-09-194-002-341	3.9	69	Sequence 341, App
1311	108	2	US-09-949-002-535	3.9	69	Sequence 535, App
1312	127	2	US-09-902-540-11829	3.9	69	Sequence 11829, A
1313	127	1	US-08-378-939-30	3.9	69	Sequence 30, Appl
1314	156	2	US-09-136-315-4	3.9	69	Sequence 4, Appli
1315	243	2	US-08-821-994-42	3.9	69	Sequence 42, Appl
1316	269	2	US-09-107-532A-6856	3.9	69	Sequence 6856, Ap
1317	329	1	US-08-727-111-3	3.9	69	Sequence 3, Appli
1318	329	2	US-08-651-200-18	3.9	69	Sequence 18, Appl
1319	329	2	US-09-303-040-6	3.9	69	Sequence 6, Appli
1320	329	2	US-09-710-279-414	3.9	69	Sequence 414, App
1321	331	2	US-09-134-001C-5258	3.9	69	Sequence 5258, Ap
1322	332	2	US-08-646-561-26	3.9	69	Sequence 26, Appl
1323	335	2	US-09-902-540-11829	3.9	69	Sequence 11829, A
1324	355	1	US-08-875-811-41	3.9	69	Sequence 41, Appl
1325	355	1	US-08-875-811-49	3.9	69	Sequence 49, Appl
1326	355	1	US-08-875-811-64	3.9	69	Sequence 64, Appl
1327	357	2	US-09-949-016-9074	3.9	69	Sequence 9074, Ap
1328	358	2	US-08-875-811-45	3.9	69	Sequence 45, Appl
1329	358	1	US-08-875-811-51	3.9	69	Sequence 51, Appl
1330	360	2	US-08-875-811-47	3.9	69	Sequence 47, Appl
1331	379	2	US-08-875-811-43	3.9	69	Sequence 43, Appl
1332	383	2	US-09-079-030-82	3.9	69	Sequence 82, Appl
1333	408	2	US-09-248-796A-17517	3.9	69	Sequence 17517, A
1334	408	2	US-09-499-662-9	3.9	69	Sequence 9, Appli
1335	464	2	US-08-030-175-42	3.9	69	Sequence 42, Appl
1336	467	2	US-09-220-151-16	3.9	69	Sequence 16, Appl
1337	468	2	US-08-113-118-16	3.9	69	Sequence 16, Appl
1338	468	1	US-08-473-446-16	3.9	69	Sequence 16, Appl
1339	468	3	US-10-026-140-2	3.9	69	Sequence 2, Appli
1340	514	2	US-09-800-729-124	3.9	69	Sequence 124, App

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#	Num	Cnt	Application No.	Score	%	Sequence
1341	519	2	US-08-996-338-21	3.9	69	Sequence 21, Appl
1342	519	2	US-09-556-972-21	3.9	69	Sequence 21, Appl
1343	523	2	US-08-606-505B-67	3.9	69	Sequence 67, Appl
1344	523	2	US-09-616-990-67	3.9	69	Sequence 67, Appl
1345	537	1	US-08-604-333-4	3.9	69	Sequence 4, Appli
1346	537	2	US-09-110-618-4	3.9	69	Sequence 4, Appli
1347	537	2	US-09-173-151A-29	3.9	69	Sequence 29, Appl
1348	537	2	US-09-578-178-4	3.9	69	Sequence 4, Appli
1349	537	2	US-09-577-806-4	3.9	69	Sequence 4, Appli
1350	542	3	US-09-621-502-8	3.9	69	Sequence 8, Appli
1351	542	1	US-10-157-447-4	3.9	69	Sequence 4, Appli
1352	542	1	US-08-140-729A-5	3.9	69	Sequence 5, Appli
1353	542	1	US-08-546-666-5	3.9	69	Sequence 5, Appli
1354	542	1	US-08-916-745-5	3.9	69	Sequence 5, Appli
1355	542	1	US-08-663-808-4	3.9	69	Sequence 4, Appli
1356	542	2	US-09-042-929-5	3.9	69	Sequence 5, Appli
1357	542	2	US-09-546-661-5	3.9	69	Sequence 5, Appli
1358	542	2	US-09-042-960-5	3.9	69	Sequence 5, Appli
1359	542	2	US-09-198-650-5	3.9	69	Sequence 5, Appli
1360	542	2	US-09-332-740-4	3.9	69	Sequence 4, Appli
1361	542	2	US-09-042-913-5	3.9	69	Sequence 5, Appli
1362	542	2	US-09-188-496-4	3.9	69	Sequence 4, Appli
1363	542	2	US-09-042-937-5	3.9	69	Sequence 5, Appli
1364	542	2	US-09-368-282-4	3.9	69	Sequence 4, Appli
1365	542	2	US-09-566-708A-4	3.9	69	Sequence 4, Appli
1366	542	2	US-09-042-709A-5	3.9	69	Sequence 5, Appli
1367	542	2	US-09-227-614-5	3.9	69	Sequence 5, Appli
1368	542	2	US-09-949-016-6462	3.9	69	Sequence 6462, Ap
1369	542	2	(illegible)	3.9	69	(illegible)
1370	542	2	(illegible)	3.9	69	(illegible)
1371	542	2	(illegible)	3.9	69	(illegible)
1372	543	2	US-09-949-016-10085	3.9	69	Sequence 10085, A
1373	561	2	US-09-198-452A-744	3.9	69	Sequence 744, Appl
1374	584	2	US-09-911-909B-14	3.9	69	Sequence 14, Appl
1375	627	2	US-09-303-518D-456	3.9	69	Sequence 456, App
1376	657	2	US-08-508-761B-2	3.9	69	Sequence 2, Appli
1377	673	2	US-09-196-387-8	3.9	69	Sequence 8, Appli
1378	673	2	US-09-841-835-8	3.9	69	Sequence 8, Appli
1379	688	2	US-09-071-035-464	3.9	69	Sequence 464, App
1380	688	2	US-10-206-576-464	3.9	69	Sequence 464, App
1381	698	2	US-10-094-749-2645	3.9	69	Sequence 2645, Ap
1382	712	2	US-09-949-016-10600	3.9	69	Sequence 10600, A
1383	745	2	US-09-308-345A-48	3.9	69	Sequence 48, Appl
1384	821	2	US-09-543-681A-7277	3.9	69	Sequence 7277, Ap
1385	851	2	US-09-949-016-6954	3.9	69	Sequence 6954, Ap
1386	919	2	US-09-438-185A-704	3.9	69	Sequence 704, App
1387	924	2	US-10-104-047-2435	3.9	69	Sequence 2435, Ap
1388	928	2	US-09-196-387-10	3.9	69	Sequence 10, Appl
1389	949	2	US-09-841-835-10	3.9	69	Sequence 10, Appl
1390	949	2	US-10-094-749-2631	3.9	69	Sequence 2631, Ap
1391	1034	2	US-09-215-694-7	3.9	69	Sequence 7, Appli
1392	1068	2	US-10-109-310-7	3.9	69	Sequence 7, Appli
1393	1068	2	US-09-196-387-2	3.9	69	Sequence 2, Appli
1394	1327	2	US-09-841-835-2	3.9	69	Sequence 8, Appli
1395	1327	1	US-09-972-115A-8	3.9	69	Sequence 458, Appl
1396	2032	2	US-09-071-035-458	3.9	69	Sequence 458, Appl
1397	2032	2	US-09-071-035-462	3.9	69	Sequence 462, App
1398	2032	2	US-10-206-576-466	3.9	69	Sequence 466, App
1399	2032	2	US-10-206-576-458	3.9	69	Sequence 458, App
1400	2032	2	US-10-206-576-462	3.9	69	Sequence 462, App
1401	2054	2	US-09-134-000C-6612	3.9	69	Sequence 6612, Ap
1402	3892	2	US-09-328-352-5503	3.9	69	Sequence 5503, Ap
1403	4536	2	US-09-180-422B-27	3.9	69	Sequence 27, Appl
1404	4536	1	US-09-079-030-1	3.9	69	Sequence 1, Appli
1405	4563	1	US-09-108-006C-1	3.9	69	Sequence 1, Appli
1406	4563	2	US-09-538-092-842	3.9	69	Sequence 842, App
1407	105	1	US-08-956-652-22	3.9	68.5	Sequence 22, Appl
1408	105	2	US-08-956-869-22	3.9	68.5	Sequence 22, Appl
1409	105	2	US-08-948-547-22	3.9	68.5	Sequence 22, Appl
1410	105	2	US-08-212-185-22	3.9	68.5	Sequence 22, Appl
1411	203	2	US-10-094-749-1808	3.9	68.5	Sequence 1808, Ap
1412	212	2	US-09-640-211A-796	3.9	68.5	Sequence 796, App
1413	217	2	US-09-291-299A-7	3.9	68.5	Sequence 7, Appli

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1414	68.5	3.9	217	7	5189147-7	Patent No. 5189147
1415	68.5	3.9	234	2	US-09-770-916-4	Sequence 4, Appli
1416	68.5	3.9	240	2	US-09-997-165-2	Sequence 2, Appli
1417	68.5	3.9	255	2	US-09-270-767-43805	Sequence 43805, A
1418	68.5	3.9	256	2	US-09-270-767-37173	Sequence 37173, A
1419	68.5	3.9	256	2	US-09-270-767-52390	Sequence 52390, A
1420	68.5	3.9	296	2	US-09-492-709A-307	Sequence 307, App
1421	68.5	3.9	306	2	US-09-171-945-95	Sequence 95, Appl
1422	68.5	3.9	306	2	US-09-910-059-95	Sequence 95, Appl
1423	68.5	3.9	310	1	US-08-078-683A-3	Sequence 3, Appli
1424	68.5	3.9	310	2	US-08-488-199-4	Sequence 4, Appli
1425	68.5	3.9	310	2	US-08-471-970A-3	Sequence 3, Appli
1426	68.5	3.9	310	2	US-09-723-677B-3	Sequence 3, Appli
1427	68.5	3.9	310	2	US-09-949-016-6296	Sequence 6296, Ap
1428	68.5	3.9	313	2	US-09-700-397-4	Sequence 4, Appli
1429	68.5	3.9	322	2	US-09-134-000C-6292	Sequence 6292, Ap
1430	68.5	3.9	362	2	US-09-949-016-9134	Sequence 9134, Ap
1431	68.5	3.9	376	2	US-09-270-767-42614	Sequence 42614, A
1432	68.5	3.9	388	1	US-08-429-742-4	Sequence 4, Appli
1433	68.5	3.9	421	2	US-09-902-540-14796	Sequence 14796, A
1434	68.5	3.9	457	2	US-08-328-500-9	Sequence 9, Appl
1435	68.5	3.9	458	2	US-09-039-555B-15	Sequence 15, Appl
1436	68.5	3.9	462	1	US-08-417-495-5	Sequence 5, Appli
1437	68.5	3.9	462	2	US-08-284-391B-5	Sequence 5, Appli
1438	68.5	3.9	462	2	US-09-218-950-5	Sequence 5, Appli
1439	68.5	3.9	462	2	US-08-394-388A-5	Sequence 5, Appli
1440	68.5	3.9	462	5	PCT-US92-01785-5	Sequence 5, Appli
1441	68.5	3.9	462	5	PCT-US95-00454-5	Sequence 5, Appli
1442	68.5	3.9	482	2	US-09-248-796A-17755	Sequence 17755, A
1443	68.5	3.9	503	2	US-09-920-262A-9	Sequence 9, Appli
1444	68.5	3.9	504	2	US-10-029-180-6	Sequence 6, Appli
1445	68.5	3.9	508	2	US-10-104-047-3233	Sequence 3233, Ap
1446	68.5	3.9	522	2	US-09-270-767-43072	Sequence 43072, A
1447	68.5	3.9	538	2	US-08-994-076-2	Sequence 2, Appli
1448	68.5	3.9	538	2	US-09-643-476-2	Sequence 2, Appli
1449	68.5	3.9	542	1	US-08-246-583-3	Sequence 3, Appli
1450	68.5	3.9	542	2	US-09-636-791A-5	Sequence 5, Appli
1451	68.5	3.9	542	2	US-09-538-092-672	Sequence 672, App
1452	68.5	3.9	542	2	US-09-494-994-12	Sequence 12, Appl
1453	68.5	3.9	589	2	US-08-991-862-2	Sequence 2, Appli
1454	68.5	3.9	589	2	US-09-813-156-2	Sequence 2, Appli
1455	68.5	3.9	589	2	US-09-456-886-2	Sequence 2, Appli
1456	68.5	3.9	589	2	US-08-824-647-2	Sequence 2, Appli
1457	68.5	3.9	589	2	US-09-880-842-2	Sequence 2, Appli
1458	68.5	3.9	613	2	US-09-171-945-113	Sequence 113, App
1459	68.5	3.9	613	2	US-09-910-059-113	Sequence 113, App
1460	68.5	3.9	628	2	US-10-101-464A-917	Sequence 917, App
1461	68.5	3.9	636	2	US-09-907-794A-175	Sequence 175, App
1462	68.5	3.9	636	2	US-09-905-125A-175	Sequence 175, App
1463	68.5	3.9	636	2	US-09-902-775A-175	Sequence 175, App
1464	68.5	3.9	636	2	US-09-906-700-175	Sequence 175, App
1465	68.5	3.9	636	2	US-09-903-603A-175	Sequence 175, App
1466	68.5	3.9	636	2	US-09-904-920A-175	Sequence 175, App
1467	68.5	3.9	636	2	US-09-907-064-175	Sequence 175, App
1468	68.5	3.9	636	2	US-09-905-381A-175	Sequence 175, App
1469	68.5	3.9	636	2	US-09-906-618-175	Sequence 175, App
1470	68.5	3.9	636	2	US-09-906-646-175	Sequence 175, App
1471	68.5	3.9	636	2	US-09-904-462-175	Sequence 175, App
1472	68.5	3.9	636	2	US-09-902-736A-175	Sequence 175, App
1473	68.5	3.9	636	2	US-09-906-722A-175	Sequence 175, App
1474	68.5	3.9	636	2	US-09-905-449-175	Sequence 175, App
1475	68.5	3.9	636	2	US-09-903-562B-175	Sequence 175, App
1476	68.5	3.9	636	2	US-09-906-679A-175	Sequence 175, App
1477	68.5	3.9	636	2	US-09-907-841-175	Sequence 175, App
1478	68.5	3.9	677	2	US-09-270-767-45699	Sequence 45699, A
1479	68.5	3.9	679	2	US-09-949-016-7268	Sequence 7268, Ap
1480	68.5	3.9	714	2	US-09-107-532A-4099	Sequence 4099, Ap
1481	68.5	3.9	822	2	US-09-252-991A-29534	Sequence 29534, A
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1491	68.5	3.9	1253	2	US-08-506-296B-14	Sequence 14, Appl
1492	68.5	3.9	1315	2	US-08-899-595-3	Sequence 3, Appli
1493	68.5	3.9	1453	1	US-08-308-872B-6	Sequence 6, Appli
1494	68.5	3.9	1686	2	US-09-355-160D-2	Sequence 2, Appli
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1496	68	3.8	177	2	US-09-543-681A-5402	Sequence 5402, Ap
1497	68	3.8	242	2	US-09-479-614-20	Sequence 20, Appl
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ALIGNMENTS

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; APPLICANT: Ashkenazi, Avi J.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Db  181  PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL  240

Qy  241  FVLGLFLWFLKRERQEEYIEEKGRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA  300
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RESULT 2
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; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
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; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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US-09-997-333-253
; Sequence 253, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C27
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;   PRIOR APPLICATION NUMBER: 60/091982
;   PRIOR FILING DATE: 1998-07-07
;   PRIOR APPLICATION NUMBER: 60/092182
;   PRIOR FILING DATE: 1998-07-09
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Matches 335;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    121  VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL  180
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Qy    241  FVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA  300
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RESULT 4
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;   Sequence 253, Application US/09992598
;   Patent No. 6956108
;   GENERAL INFORMATION:
;   APPLICANT: Ashkenazi,Avi J.
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Botstein,David
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Eaton,Dan L.
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Fong,Sherman
;   APPLICANT: Gerber,Hanspeter
;   APPLICANT: Gerritsen,Mary E.
;   APPLICANT: Goddard,Audrey
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;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Grimaldi,J.Christopher
;   APPLICANT: Gurney,Austin L.
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;   APPLICANT: Napier,Mary A.
;   APPLICANT: Pan,James
;   APPLICANT: Paoni,Nicholas F.
;   APPLICANT: Roy,Margaret Ann
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe,Colin K.
;   APPLICANT: Williams,P. Mickey
;   APPLICANT: Wood,William I.
;   APPLICANT: Zhang,Zemin
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2730P1C20
;   CURRENT APPLICATION NUMBER: US/09/992,598
;   CURRENT FILING DATE: 2001-11-14
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;   PRIOR FILING DATE: 1997-11-24
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;   PRIOR APPLICATION NUMBER: 60/083322
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Qy     1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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RESULT 5
US-09-989-735-253

Sequence 253, Application US/09989735
Patent No. 6972185
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
APPLICANT: Desnoyers,Luc
APPLICANT: Eaton,Dan L.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
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TITLE OF INVENTION: Acids Encoding the Same
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RESULT 6
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; Sequence 253, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy,Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C60
; CURRENT APPLICATION NUMBER: US/09/989,726
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1997-06-16
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Thu Mar 29 08:56:38 2007

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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09
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;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT: Baker, Kevin P.
;  APPLICANT: Botstein, David
;  APPLICANT: Desnoyers, Luc
;  APPLICANT: Eaton, Dan L.
;  APPLICANT: Ferrara, Napoleone
;  APPLICANT: Fong, Sherman
;  APPLICANT: Gerber, Hanspeter
;  APPLICANT: Gerritsen, Mary E.
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Godowski, Paul J.
;  APPLICANT: Grimaldi, J.Christopher
;  APPLICANT: Gurney, Austin L.
;  APPLICANT: Kljavin, Ivar J.
;  APPLICANT: Napier, Mary A.
;  APPLICANT: Pan, James
;  APPLICANT: Paoni, Nicholas F.
;  APPLICANT: Roy, Margaret Ann
;  APPLICANT: Stewart, Timothy A.
;  APPLICANT: Tumas, Daniel
;  APPLICANT: Watanabe, Colin K.
;  APPLICANT: Williams, P. Mickey
;  APPLICANT: Wood, William I.
;  APPLICANT: Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION: Acids Encoding the Same
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;  PRIOR FILING DATE: 1997-06-16
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; ; PRIOR FILING DATE: 1998-07-02
; ; PRIOR APPLICATION NUMBER: 60/091978
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; ; PRIOR FILING DATE: 1998-07-09
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Query Match             100.0%;  Score 1772;  DB 3;  Length 335;
Best Local Similarity   100.0%;
Matches  335;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIWTFNTTPL 60
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Qy    121 VLHVEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Qy    181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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RESULT 8
US-09-989-728-253
; Sequence 253, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/090863          ;   APPLICANT:    Stewart, Timothy A.
; PRIOR FILING DATE: 1998-06-26                ;   APPLICANT:    Tumas, Daniel
; PRIOR APPLICATION NUMBER: 60/091360          ;   APPLICANT:    Watanabe, Colin K.
; PRIOR FILING DATE: 1998-07-01                ;   APPLICANT:    Williams, P. Mickey
; PRIOR APPLICATION NUMBER: 60/091478          ;   APPLICANT:    Wood, William I.
; PRIOR FILING DATE: 1998-07-02                ;   APPLICANT:    Zhang, Zemin
; PRIOR APPLICATION NUMBER: 60/091544          ;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; PRIOR FILING DATE: 1998-07-01                ;   TITLE OF INVENTION: Acids Encoding the Same
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;   APPLICANT: Ashkenazi,Avi J.               ;   PRIOR FILING DATE: 1998-06-05
;   APPLICANT: Baker,Kevin P.                 ;   PRIOR APPLICATION NUMBER: 60/088212
;   APPLICANT: Botstein,David                 ;   PRIOR FILING DATE: 1998-06-05
;   APPLICANT: Desnoyers,Luc                  ;   PRIOR APPLICATION NUMBER: 60/088217
;   APPLICANT: Eaton,Dan L.                   ;   PRIOR FILING DATE: 1998-06-05
;   APPLICANT: Ferrara,Napoleone              ;   PRIOR APPLICATION NUMBER: 60/088655
;   APPLICANT: Fong,Sherman                   ;   PRIOR FILING DATE: 1998-06-05
;   APPLICANT: Gerber,Hanspeter               ;   PRIOR APPLICATION NUMBER: 60/088734
;   APPLICANT: Gerritsen,Mary E.              ;   PRIOR FILING DATE: 1998-06-09
;   APPLICANT: Goddard,Audrey                 ;   PRIOR APPLICATION NUMBER: 60/088738
;   APPLICANT: Godowski,Paul J.               ;   PRIOR FILING DATE: 1998-06-10
;   APPLICANT: Grimaldi,J.Christopher         ;   PRIOR APPLICATION NUMBER: 60/088742
;   APPLICANT: Gurney,Austin L.               ;   PRIOR FILING DATE: 1998-06-10
;   APPLICANT: Kljavin,Ivar J.               ;   PRIOR APPLICATION NUMBER: 60/088810
;   APPLICANT: Napier,Mary A.                 ;   PRIOR FILING DATE: 1998-06-10
;   APPLICANT: Pan,James
;   APPLICANT: Paoni,Nicholas F.
;   APPLICANT: Roy, Margaret Ann
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Db   61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYVGIYSSSLQQPSTQEY 120

Qy  121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180
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Db  121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSIL 180

Qy  181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
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Db  181 PISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240

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Db  241 FVLGLFLWFLKRERQEBYIEBKKQRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300

Qy  301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 10
US-09-997-653-253
; Sequence 253, Application US/09997653
; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
```

APPLICANT: Ferrara,Napoleone
APPLICANT: Fong,Sherman
APPLICANT: Gerber,Hanspeter
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Grimaldi,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
CURRENT FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/090431
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PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24

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Db             301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335


RESULT 11
US-09-989-293A-253
; Sequence 253, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi,Avi J.
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Botstein,David
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Eaton,Dan L.
;   APPLICANT: Ferrara,Napoleone
;   APPLICANT: Fong,Sherman
;   APPLICANT: Gerber,Hanspeter
;   APPLICANT: Gerritsen,Mary E.
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;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Grimaldi,J.Christopher
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Kljavin,Ivar J.
;   APPLICANT: Napier,Mary A.
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;   APPLICANT: Paoni,Nicholas F.
;   APPLICANT: Roy, Margaret Ann
;   APPLICANT: Stewart,Timothy A.
;   APPLICANT: Tumas,Daniel
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William I.
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;   TITLE OF INVENTION: Acids Encoding the Same
;   FILE REFERENCE: P2730PIC66
;   CURRENT APPLICATION NUMBER: US/09/989,293A
;   CURRENT FILING DATE:  2001-11-20
;   PRIOR APPLICATION NUMBER: 60/049787
;   PRIOR FILING DATE: 1997-06-16
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;   PRIOR FILING DATE: 1998-07-07
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;   PRIOR FILING DATE: 1998-07-09
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Best Local Similarity 100.0%;   Pred. No. 4.4e-183;
Matches  335;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps    0;

Qy     1 MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
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; PRIOR APPLICATION NUMBER: 60/090246   Qy   61 VTIQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEY 120
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Db 181 PISWRWGSDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSL 240
Qy 241 FVLGLFLWFLKRERQEBYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
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Db 241 FVLGLFLWFLKRERQEBYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPA 300
Qy 301 NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI 335
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RESULT 12
US-09-513-999C-4472
; Sequence 4472, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
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; OTHER INFORMATION: seq LIYILWQLTGSAA/SG
US-09-513-999C-4472

Query Match   28.1%; Score 498; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.5e-46;
Matches   97; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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RESULT 13
US-09-949-016-6428
; Sequence 6428, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6428
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6428

Query Match   20.5%; Score 362.5; DB 2; Length 328;
Best Local Similarity 31.5%; Pred. No. 2.3e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

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; Sequence 483, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
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; EARLIER APPLICATION NUMBER: 60/047,633

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; EARLIER FILING DATE: 1997-10-02
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; ORGANISM: Human
US-09-949-016-7327

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Best Local Similarity   31.5%;   Pred. No. 2.3e-30;
Matches  107;  Conservative  55;  Mismatches 143;   Indels  35;   Gaps  10;

Qy   14 LWQL-----TGSAASGPVKELV--GSVGGAVTFPLK-SKVKQVDSIVWTFNTTPLVTIQ 64
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Db  126 LQIYRRLGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNWSPLGE------EGNVLQ 179
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Db  180 IFQTPEDQELTYTCTAQNPVSNN-SDSISARQLCADIAMGFRTHHTGLLSVLAMFFLLVL 238
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RESULT 15
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; Sequence 7327, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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